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GENETICAL IMPROVEMENT OF YIELD AND QUALITY TRAITS OF SOME TOPCROSSES OF RICE

By

Nadia Atef Ibrahim Abdallah Taalab

B.Sc. Agric. Sci. (Agronomy), Fac. Agric.,
Benha University, 2022.

. **A Thesis submitted in partial fulfillment of**

The requirements for the degree of

In

Agricultural Science
(Crop Breeding)

Department of Agronomy

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Approval Sheet

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ABSTRACT

This work was undertaken at the Farm of Rice Research and Training Center. (RRTC), Sakha, Kafr El-Sheikh, Egypt, to investigate the gene action of some morphophysiological, yield and its attributing traits as well as quality traits during 2023 and 2024 seasons. The plant materials of this work included six parental varieties, i.e., Sakha104, Sakha106, GZ11332, Sakha108, Sakha109, Sakha101 and 4 testers Viz., IHL17, IHL65, IHL175, Super303 of rice. Combining ability was estimated according to Kempthorne (1954). The mean squares of genotypes and their partitions were significant for studied traits. Yield and its associated qualities were inherited due to non-additive gene activity. The most desirable SCA effects were obtained by crosses Sakha108xIHL17 for hulling% and head rice recovery. The highest SCA effects for milling% and grain shape were detected by the crosses Sakha106xIHL175 and GZ11332xSuper303, respectively. The highest heterosis relative to Mid-Parent and better -Parent were detected by crosses Sk106xSR303 for hulling%, the cross Sakha109xIHL65 for head rice recovery, and the cross GZ11332xSuper303 for grain shape. Regarding milling%, the best heterotic effect was detected by the cross Sakha109xSR303 relative to mid parent and the cross Sakha109xIHL65 relative to better parent. From the previous results, the line Saka 109 and tester Super 303 were the best parent. The cross Sakha 109 × Super 303 was the most desirable value for grain yield plant and most of its attribute traits. As a result, this cross is promising and may be applied in upcoming rice breeding initiatives to improve yield potentiality and quality.

Key wards: Combining ability – quality traits – Heterosis – yield and its components traits.

List Of Contents

List of Tables

List of Figures

List of Abbreviations

Abbreviation	Meaning
EAS	Economic Affairs Sector.
RRTC	Rice Research and Training Center.
RTTC	Rice Technology and Training Center.
t/h	Ton per hectares.
IHL	International hybrid line.
SK	Sakha
SR	Super
GCA	General combining ability.
SCA	Specific combining ability.
S. E	Stander error
M.p	Mid parent.
B. P	Better parent.
L.S. D	Least Significant Difference.
Mg^{2+}	Magnesium
Na^{+}	Sodium
SO_4^{2-}	Sulfate
K_2O	Potassium Oxide
Ca^{2+}	Calcium
CEC	Cation Exchange Capacity

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INTRODUCTION

1.INTRODUCTION

In Egypt and around the world, rice (Oryza sative L.) (2n=24) is regarded as one of the major cereal crops. In terms of cultivated area, it comes in third place in Egypt and the world, behind maize and wheat. In Egypt the cultivated area is 553.200 hectares of rice. The yield is 3.900.000 tons of milled rice and 5.200.000 tons of rough rice in 2024, with an average of 9.44 t/ha. The majority of the world's population is fed by rice, which is primarily grown in Egypt and Southeast Asia. (**EAS, 2024).**

Due to the issue of water scarcity, the agricultural land is now restricted to the Nile River Delta. Higher imports are the result of both population growth and a decline in rice-growing land. Wide, short-grain rice with low amylose and high bleaching clearance is preferred by Egyptian consumers. The market and consumer preferences influence the quality criteria for rice. To narrow the gap between production and demand, increasing yield and its component is the only option left.

Improving rice productivity under different stress conditions by combining conventional breeding methods with its modern techniques to obtain desirable promising genotypes for yield and its components. It is of great importance to take these points into consideration. The yield and its components are determined by No. of panicles / plant, panicle weight, spikelet fertility, 1000grain weight, grain yield/plant and harvest index.

High quality is a worldwide scientific issue that has not gotten enough attention during the rice variety breeding process. To boost output at the national agricultural level and promote the beginning of commercial and industrial application, consideration must be given to the yield and quality of rice. Improving the quality of rice and grain yield has grown in importance because higher rice grain quality translates into higher prices.

The quality of rice can be determined by grain length, grain width, and grain shape (length/width ratio). In addition to hulling, milling and head rice recovery.**Kumar, et al., (2024).**

Egypt has witnessed improvements in rice varieties with evidence of success in the development of early maturing varieties having higher grain yield and better grain quality. **Ayuba, et al., (2022).**

Selecting the appropriate parents is the cornerstone of an effective breeding program. The study of Combining ability benefits to determine optimal combiners that are involved in hybridization to exploit heterosis and the effect of gene action **Santhiya et al., (2024).**

The design of line × tester is used to scrutinize combining ability (GCA) according to Kempthorne, (1957). General combining ability explains additive gene action, while specific combining ability explains hybrid performance related to non- additive gene action. The presence of non-additive genetic variance is the primary justification for initiating the hybrid program. Additive gene action is important for breeders which reflects the selection program in breeding crops **Kumar, et al., (2024).**

Among many genetic approaches being explored to break the yield barrier in rice and increased productivity, hybrid rice technology appears to be the most feasible and readily adaptable one **Abd El-Aty et al., (2023).**

Heterosis is the first generation's superiority over its parents. It has aided plant breeders and geneticists in creating cultivars for a variety of crops, increasing yields by 15% to 20% over market versions. The hybridization program is initiated based on non-additive gene action. While negative heterosis is significant with regard to blooming days, etc., positive heterosis is significant with regard to attributes like grain yield, grain weight, etc. **El-Mowafi et al (2022).**

Therefore, the main objectives of this investigation were to:

1. Study gene action for morphophysiological, yield and some quality traits in rice and add new in the field of rice breeding.

2. Estimate some of the appearance quality traits for some top crosses and parents studied rice.

3. Analyze both types of combining ability for morphophysiological, yield and some quality traits in rice.

4. Determine heterosis relative to mid-parent and better-parent for all traits studied.

REVIEW OF LITERATU

2. REVIEW OF LITERATURE

The available review related to the current study including gene action and heterosis of some yield and quality traits in rice will be elucidated as follows: 2.1. Combining ability and gene action.

2.2. Heterosis.

2.3. Quality characteristics.

2.1. Combining ability and gene action.

Ariful Islam *et al*., (2015) obtained 80 crosses from the hybridization of five females and sixteen males in the line x tester model to study gene action for 5 traits in rice. Genotypes mean squares were significantly detected for the five traits, revealing that these genotypes were diversified. One female parent and three pollen parents expressed significant and positive GCA effects on pollen fertility. Significant SCA impacts were perceived for earliness (15 crosses), days to maturity (16 crosses), and grain yield (52 crosses).

Mohamed *et al*., (2016) evaluated thirty crosses of rice for yield and some of its components. They concluded that SCA effects were more important than GCA ones, consequently, non-additive gene action was predominant for all traits except 1000 grain weight. One parent (Pant Sugandh Dhan--17) was the best general combiner, while the highest SCA effects were detected for seed yield in three crosses.

Babu and Sreelakshmi (2018) studied the combining ability of ten important traits including grain yield in twenty-one crosses of rice. They observed the preponderance of dominance and epistasis variance in controlling grain yield and additive variance for other studied traits. Five parents demonstrated the importance of GCA effects, while three crosses (Samba-Mahsuri x NLR 33637, Swarnamukhi x Bharani and

Erramallelu x Samba-Mahsuri) were the best specific combiners for most attributes.

Saravanan *et al.*, (2018) applied a line x tester pattern where eight lines were crossed to four testers to estimate combining ability for six traits in rice. Results showed a great deal of variability among genotypes studied for all features. Moreover, parental line KR-09009 and tester ASD-19 were the best combiners for most traits, while three crosses were the best specific combiners in this study.

Yuga *et al.*, (2018) made a cross between 9 males and 3 females to get valuable information about gene action for yield and its attributable traits, in rice. The resultant 27 top crosses alongside their parents were assessed for combining ability analysis. Four parental lines seemed to be good combiners for seven traits including grain yield, whereas four crosses exhibited worthy SCA effects for grain yield.

Kiani (2019) evaluated six F1 crosses alongside their four parents to estimate gene action for important traits in rice. He recounted that additive gene action was predominant for grain length, while both types of gene action were important for most studied traits. Conversely, non-additive was predominant for tiller number.

Singh *et al.*, (2019) scrutinized thirty-nine crosses resulting from the hybridization between twelve lines and three testers in L x T mating pattern. Twelve agronomical traits of rice were involved in this study. Variances of lines were significant for five out of 12 traits studied, while significant differences were detected for all attributes. Testers mean squares were not significant for all traits studied. Variance due to specific combining was significant for all characters, revealing the predominance of dominance and epistasis in controlling all attributes.

Abd El-Aty *et al.* (2020) evaluated twenty-one crosses for both types of combining abilities and insinuated the importance of δ^2 SCA in controlling all traits studied. Consequently, the significance of the role of selection in advanced generation to improve the studied traits. The parent Sakha 103 exhibited the best GCA for plant height. Four crosses were the best specific combiners for the attributes studied.

Buelah *et al*., (2020) crossed four males with six females to generate forty-four crosses for studying the combining ability of grain yield and other related traits in rice. Data unveiled that SCA was more imperative than GCA for most attributes. This result clarified the substantial role of non-additive effects on the studied traits. Consequently, heterosis breeding became an efficient tool for improving these traits. Five parents expressed their ability as good general combiners for most traits. Moreover, eight crosses were superior since they had the best SCA effects for yield and most of its components.

Aamer and Ibrahim (2020) evaluated fifteen crosses of rice for combining ability of eight traits including grain yield plant^{-1}. They found that variance due to GCA was more important than SCA for yield and the other seven traits. Two parents (Giza 178 and Giza 179) possessed meaningful GCA effects for five traits. Seven crosses exhibited the best SCA effects for grain yield and some other traits.

Abo-Yousef *et al*., (2020) identified superior general and specific combiners from forty crosses resulting from the crossing between 4 males with 10 testers. Differences among genotypes reached a level of significance for all attributes. The non-additive genetic component had a major role in controlling the studied traits. One parent (IR58025A) possessed the possibility to be a good combiner for most traits. The most desirable values of SCA were detected by four crosses for grain yield plant^{-1}.

Gaballah *et al*., (2021) studied the combining ability of fifteen traits in rice from L x T mating design using four males and five females. Their data revealed that the cross WTSC9059 × Sakha101 gave the highest yield, followed by the cross WTSC9039 × Sakha102, recording 14.04 and 12.04 t/ha, respectively, whereas the lowest yield was recorded for the two crosses WTSC9039 × Sakha105, and long ping × Sakha107, being 3.01 t/ha. Two lines, namely, WTSC9059 and Longping; and three testers, viz, Sakha 101, Sakha 102 and Sakha 108 were the superlative combiners for grain yield.

Savi *et al*., (2021) studied the combining ability of five traits in fifty-five crosses in rice and found that both types of genetic components were participating in the inheritance of all traits. However, the additive component was predominant where the GCA/ SCA ratio was higher than unity for all attributes. Three parental lines, viz, M 57, IRAT-256, and Salama M 19 displayed the most appropriate GCA effects for GY, accentuating the possibility of using these materials in rice breeding programs for higher yield potentiality

Abd El-Aty *et al*., (2022) determined the gene action controlling ten important attributes of rice, including grain yield plant^{-1}. The evaluation of the twenty-one crosses and their parents clarified that genotypes differ significantly for all traits. Moreover, the δ2 SCA value was much higher than that of δ2 GCA for most attributes, proving the importance of dominance and epistasis in controlling traits studied. Three parents were superior for GCA effects, while five crosses were appropriate specific combiners for most traits.

Ayuba *et al*., (2022) estimated the two types of combining ability for ten traits of rice from 21 F1 crosses. Their results illuminated the prominent level of diversity among the studied crosses for all attributes. It was found that whereas dominance was higher for yield per plant, additive variance predominated for plant heights and productive tillers. For the ten attributes studied, the GCA status was higher for four parents. Four F1 crosses expressed higher SCA values for most agronomical traits.

Bayoumi *et al.* (2022) scrutinized fifteen crosses for combining ability resulting from L x T mating pattern in which five lines were crossed to three Tester. Results indicated that differences among genotypes studied were significant for all attributes. Also, δ^2 SCA was higher than δ^2 GCA for all revealing the significant role of the non-additive genetic component in controlling traits studied. Parents Sakha 107 and Sakha 108 were the best combiners for earliness and grain yield, respectively. In the meantime, the cross Sakha 108 x Sakha 101 for earliness and the cross Giza-182 x Giza-179 for grain yield produced the best SCA scores.

El-Badawy *et al.*, (2022) chose a set of eight parents (5 lines and 3 testers) in L x T pattern, and the fifteen hybrids produced were examined for combining ability. The results showed that δ2 SCA outperformed δ2 GCA for all traits except plant height. One parent (GZ 1368) demonstrated the best GCA for grain yield. Furthermore, just one cross shown the best SCA benefits on grain yield.

El-Gammaal *et al.*, (2022) assessed both types of the combining ability of six traits in rice including grain yield through L x T mating approach with six lines and three testers. Three crosses demonstrated the best performance for the six studied attributes. Statistical analysis revealed that δ2 SCA variance was larger than δ2 GCA for four traits confirming the importance of dominance and epistasis in governing the traits studied. The most excellent general combiners were GZ10101-5 (for No. of panicles/ plant), Sakha 108 (panicle length), Sakha 107 (1000 grain weight, grain yield plant^{-1}, and fertility%). The most desirable specific combiners were detected for the number of panicle plant^{-1}, panicle length, panicle weight, 1000 grain weight, and grain yield plant^{-1}, by the crosses Sakha 107 x Hispagran, Sakha 108 x Sakha Super 300, Sakha 108 x Sakha Super 300, GZ 10101 S x Sakha-Super 300, and Skaha 108 x Sakha-Super 300, respectively.

El-Sharnobi *et al*., (2022) crossed 6 lines with 4 testers in L x T mating design to assess the genetic components of twelve traits in rice. Mean squares due to genotypes were highly significant for all studied traits. Moreover, two parents, namely, PR-78 and IR-5805A recorded the most desirable GCA for grain yield, while the best combiners for bio-mass were two crosses (PR-78 7 IR-6965A). The cross IR069625A x PR2 exhibited the best SCA effects for grain yield.

Garkoti and Pandy (2022) used line x tester model with 12 lines and 3 testers to find out the magnitude of the two main components of genetic variance (GCA & SCA) for fourteen traits in rice. Their results confirmed that most non-additive genetic components govern all attrib-utes except total tiller/ plant and grain breadth. They added that four lines (HPR-2884, HPR-2871, HPR-2873, and HPR-2889) exhibited sig-nificant GCA effects, while four crosses bared desirable SCA for most traits.

Neupane (2022) used 3 sets of crosses to assess the combining ability of eight traits of rice. The first set consisted of two lines and four testers, set 2 comprised of 3 lines and two testers, while set 3 incorpo-rated two lines and two testers. The resulting 18 crosses showed maxi-mum variability for all studied attributes. For days to flowering, one par-ent (Himali) and one cross (Khumal-8 X Sugandha 2) were the best all over the three sets of crosses. Regarding effective tillers, the parent Manjushree-2 expressed the highest GCA, whereas the cross Khumal-8 X IR775-39-80-2-2-2 exhibited the best SCA values. For 1000 grain weight, the most applicable importance for GCA and SCA were observed for the parent Sugandha 2 and the cross Khumal-8 x Sugandha 2, respectively all over the three sets.

Shrivastav *et al.*, (2022) evaluated combining ability for eighteen attributes in rice through line x tester analysis. They deduced that the studied genotypes were incongruous for all traits, consequently genetic improvement in rice could be achieved. Variances due to SCA were higher than GCA for most studied characteristics. Ten parents out of twenty-four expressed significant and positive GCA effects for grain yield and some contributing traits. Also, twenty-three crosses out of sixty-three were of great value for SCA effects for grain yield.

Sunny *et al.*, (2022) conducted an experiment to assess the combining ability in twenty-one crosses of rice. They found that mean squares due to both components of combining ability were extremely significant for all studied traits. However, the GCA/ SCA ratio was less than the unity demonstrating the importance of non-additive gene action for all characters. The most beneficial GCA effects for grain yield and other traits were noticed for the variety Pusa Basmati 1. Meanwhile, the cross Baskota × Tulaipanji exhibited positive and significant SCA effect for seed yield per plant.

Abd-Aty *et al.*, (2023) estimated both types of combining abilities of some physiological, chemical and yield components through L x T mating fashion. They crossed seven lines with three testers, and the resultant crosses, alongside their parents, were evaluated during the 2017 and 2018 seasons. For every attribute under study, notable variations were found between the lines, testers, and lines x tester. The dominant genetic component was more important than the additive genetic one for governing all studied qualities. Two parents and three crosses exhibited desirable GCA and SCA effects for most attributes studied.

Al-Daej (2023) evaluated 21 crosses for six traits regarding combining ability in rice. He postulated that the studied attributes differ significantly from each other and the mean squares due to both types of combining abilities were highly significant presuming the role of both types of gene action in controlling the studied traits. The best SCA effects for grain yield were Sakha101 x Hassawi-1, Giza175 x Sakha103, and Gz9577 x Giza175.

Das *et al*., (2023) crossed four maintainers (lines) with eleven restorers (testers) in L x T mating approach to estimate gene action of twelve rice parameters. The prevalent role of non-additive genetic components was detected for all parameters except total number of tillers, No. of productive tillers, and kernel L/B ratio. In the meantime, one line (Jyothi) recorded the highest GCA status, and one cross (Aruna x Varsha) recorded the best SCA values for most traits.

Kumar and Pandy (2023) determined the gene action for eleven traits of rice using ten lines and three testers in line x tester pattern. The obtained thirty crosses were evaluated in CRBD with 3 replications. Statistical analysis revealed that the dominant genetic component was more important than the additive one for most attributes. Four lines and three crosses exhibited the most applicable effects for GCA and SCA, respectively for various traits.

Kushal et al., (2023) crossed eight lines with four testers in L x T mating design to evaluate combining ability for seven traits in rice involving grain yield plant^{-1}. Results asserted significant differences between lines, testers and their crosses for all traits. The ratio GCA/ SCA clarified that non-additive gene action was prevailing for panicle length, plant height, No. of productive tillers plant^{-1}, grain yield plant^{-1}, kernel length. On the other hand, the predominance of additive type of gene action was observed for 1000 grain weight, days to 50% flowering and

No. of filled grains panicle^{-1}. The parent KNM-13555 and the tester Ag-anni-MRR4 were considered as good combiners for grain yield and its attributes. Five crosses expressed superiority for SCA effects regarding grain yield plant^{-1}.

Maring *et al*., (2023) used line x tester analysis including four parental lines and 8 testers was applied to estimate genetic components for 13 traits in rice. Results revealed that one line and two testers exhibited desirable GCA effects for most attributes. However, none of the forty-five hybrids expressed favorable SCA effects for all traits.

Thakur *et al*., (2023) conducted an experiment to apprehend the nature of gene action of 11 characters of rice. To achieve their objectives, they used five males and five females in line x tester model. Except for plant height, and biological yield, non-additive gene action was prevalent for all traits under study. The superlative general combiners were line PKV-HMT and tester Pusa-1121, while two crosses were the valuable specific combiners for grain yield.

Abo-Youssef *et al*., (2024) crossed four lines with seven testers in L x T pattern to evaluate combining ability for Plant height, Number of panicles/plants, Grain yield/plant and Harvest Index % traits in rice. Their results clarified the great variability among twenty-eight crosses studied for all attributes. Dominance and epistasis were more important than additive genetic components for traits studied. One line and three testers seemed to be the best general combiners for all attributes. Moreover, eight crosses exhibited the highest significant and positive SCA effects for all attributes.

Arunkumar and Narayanan (2024) implemented an experiment with six lines and four testers to evaluate both types of combining ability for 11 morphological traits in rice. Their results revealed that non-additive gene action was predominant since mean squares due SCA were much higher than those of GCA for all traits. Three testers, namely ADT 37, ADT 43 and ADT 38 were the best among all testers for grain yield and most of their attributes. Also, three hybrids (ADT 43 x CSR 36, ADT 42 x CSR 36 and ADT 37 x CSR 36) were superior regarding SCA effects of most traits**.**

El-Naem *et al*. (2024) investigated the inheritance of yield and its related agronomic traits in a line x tester model with five lines and three testers. They mentioned that the genotypes studied had apparent variations for all studied traits. Both types of genetic components (additive and non-additive) were responsible for the inheritance of all attributes studied. Two parents, namely, 11 L236 and Giza 178 exhibited desirable GCA effects for most traits. Moreover, five crosses expressed desirable SCA for yield and some other traits.

Kumar *et al*., (2024) adopted L x T mating design with ten lines and three testers to appraise the genetic behaviour of eight traits in rice. They observed the high diverseness among studied crosses for all studied attributes. Specific combining ability predominated GCA for all traits except plant height. Consequently, non-additive was more important in governing the studied traits. One line and two testers behaved as good general combiners for most traits. Moreover, three crosses, namely CMS-64A x JGL 38156, CMS-59A × JGL 36147 and CMS-59A × JGL 36172, exhibited the best SCA values for grain yield.

Modarresi *et al*., (2024) used L x T mating approach to assess combining ability in rice where five maternal parents were crossed to three paternal parents. Variances due to genotypes alongside the components of combining abilities were significant for all attributes. However, plant height was governed by additive components, while non-additive controlled grain yield and other related attributes. For early maturity, two parents, namely, Hasani and Saleh demonstrated their superiority as good combiners.

Santhiya *et al*., (2024) applied L x T mating approach to elucidate the combining ability for nine traits in rice. They found that both components of combining abilities were significant. However, the non-additive component was predominant for most traits. Also, one parental line and two testers proved to be good combiners for yield and other attributes. Regarding SCA, two crosses, namely, CO-55 × IC-457996 and ADT-54 × IC-115439 exhibited practical value for yield potentiality in rice. Therefore, these hybrids might be prospective in rice breeding for higher productivity.

Somtochukwu and Abiodun (2024) crossed six males to seven females and the crosses were used to evaluate the combining ability of ten agronomic traits of rice. The mean value of plant height was detected for cross UPIA-2 x 234, while the lowest value for this treat was given by cross UPIA-2 x 226. Meantime, cross FARO-52 x UPN-223 followed by the cross UPIA-2 x UPN34 exhibited the best performance for grain yield. Dominance genetic variance appeared to be the highest genetic component governing the traits studied. The best combiners for plant height were UPN-268 and FARO-52, and WBK-114 for yield. Two crosses, namely, UPIA-2 x 234 and FARO-52 x UPN-257 expressed the highest SCA's.

Vennila (2024) developed twenty-four crosses from the hybridization between four testers and six lines in L x T mating pattern to assess the combining ability of ten traits in rice. Statistical analysis revealed the diversity among the germplasm used in this study. The GCA/SCA ratio was less than the unity, indicating that the non-additive component was predominant for all traits. The performance of GCA was obvious for seven parents (four males and three females). Two crosses, namely, ADT-45 x Kalurundai Samba and ADT-37 x Kahurundai Samba exhibited their performance for SCA effects.

Singh *et al.*, (2025) applied the approach of L x T analysis using seven lines and three testers to evaluate eleven traits in rice. Their results clarified the predominant role of GCA for nine out of the eleven studied attributes. Two parents, namely, DRR Dhan-62 and MTU1197 had applicable measures of GCA for early flowering. One top cross (R1853-105-1-82-1 x ISM) exhibited the most desirable SCA effects for grain panicle^{-1}, being 17.39.

2.2. Heterosis.

Sathya and Jebaraj (2015) evaluated 90 hybrids along with 21 parents in Line x Tester mating design under water stress and fully irrigated (control) conditions. They showed that, significant standard heterosis over check IR6888 and hybrid IR79156A / IR 79582-21-2-2-1R (L2 x T5) for days to 50% flowering, number of tillers per plant, panicle length, chlorophyll content, relative water content number of panicles per plant, spikelet fertility, harvest index and single plant. yield except for plant height and 100-grain weight.

Abd–El-Aty *et al.*, (2016) studied heterosis for morphological, yield and its related traits. The results revealed greater magnitude of heterosis when it measured as a deviation from mid and better parent which was observed in Short Gelotinious x Rehio rice cross for grain yield per plant.

Devi *et al.*, (2017) estimated heterobeltiosis effects for yield and quality traits in 18 cross combinations generated through Line × Tester mating design. The estimates of heterosis were low for quality traits when compared to yield and yield components. Eighteen hybrids showed significant average heterosis, heterobeltiosis and standard heterosis for grain yield / plant. The crosses Kavya × JGL19618, Kavya × CN1448-

5-2-5-5-MLD-6, MTU1075 × JGL19618, CN1774-303-313-19-8-8 × CN1448-5-2-5-5-MLD6 and HKR08-62 × CN1448-5-2-5-5-MLD6 recorded significant heterobeltiosis for grain yield/plant. Considering both yield and quality traits together HKR08-62 × CN1448-5-2-5-5-MLD6, CN1774-303-313-19-8-8 × JGL19618, HKR 08-62 × JGL19618 and MTU1075 × CR3005-230-5-50 could be isolated for possessing desirable average heterobeltiosis. Higher estimates of heterosis were observed for grain yield / plant, filled grains per panicle, test weight, plant height, head rice recovery and effective tillers, whereas estimates were low for panicle length, hulling recovery and milling recovery.

Saravanan *et al*., (2018) used thirty-two crosses to estimate standard heterosis for six agronomical traits in rice and found that one hybrid (L6 x T3) exhibited the most desirable standard heterosis for yield potentiality and other studied characteristics.

Yuga *et al*. (2018) estimated heterosis values for grain yield and other traits in 27 top crosses and obtained 20% excess of standard check variety for grain yield in five out of the studied twenty-seven crosses. They added that the studied crosses were promising and could be good breeding donors.

Gaballah *et al*., (2021) studied heterosis of fifteen traits in rice from twenty crosses. Significantly positive, better parent heterosis for grain yield was detected for eleven out of twenty crosses. Moreover, the highest paramount heterosis over better parent for yield was detected in four crosses, namely, WTSC9059 × Sakha101, WTSC9369 × Sakha101, Longping × ‘Sakha105 and WTSC9039 × Sakha102, recording 57.12 %, 66.61 %, 71.51 % and 100.00 %, respectively.

Ghidan and Khedr (2021) estimated heterosis in fifteen crosses of rice and found that 3 crosses exhibited desirable heterotic effects for days to 50% flowering and plant height. Regarding panicle length, the heterotic values ranged from 4.79 to 38.89%. Also, desirable heterosis was recognized for grain yield

Hussein (2021) estimated heterosis values in rice for yield traits and reported that the crosses viz., IRBLKM-TS-[CO] x Giza-177 and Black Rice x Sakha 101 expressed the best heterosis for grain yield over mid-parent. For earliness, the cross, Dullar x Giza-177, Black Rice x Giza-178, IRBLKM-TS-[CO]x Giza 178 and Black Rice x Giza 177 gave the most desirable mid-parent heterosis.

Abd El-Aty *et al.*, (2022) determined mid-parent heterosis from twenty-one crosses for ten characters in rice and found significant negative heterotic values for earliness in three crosses where parent Sakha 101 was crossed to each of Sakha 105, Giza 177, and Black rice 3. Also, four crosses exhibited the highest significantly negative heterotic effect for plant height. Two crosses expressed significantly positive heterosis for the trait flag leaf area. For grain yield, the most beneficial heterosis was displayed by one cross (Black rice 1 x Black rice 3), recording 55.73%. The cross Sakha 10 x Black 1 gave the most appropriate mid-parent heterosis for the harvest index.

Ayuba *et al.*, (2022) estimated mid-parent, better-parent and standard heterosis for ten agronomical traits from 21 F1 crosses. For earliness, the best heterosis values were detected for the cross FARO-57 x FARO-31 (mid-parent), FARO-64 x FARO-57 (better-parent), and FARO-26 x FARO-64 (standard heterosis). For grain yield t/ ha, the cross FARO-57 x FARO-66 exhibited the best mid-parent, better-parent and standard heterosis recording 26.84, 18.54 and 41.58%, respectively.

Bayoumi *et al.* (2022) measured heterosis in fifteen crosses of rice and found that the most beneficial mid-parent heterosis values were obtained by the crosses: Sakha 107 x Sakha 101; for 50% flowering and grain yield, Giza-182 x Giza-177; for plant height, and Giza-182 x Giza-

179; for chlorophyll content. Regarding better-parent heterosis, desirable values were detected for the crosses: Sakha-107 x Sakha-101; for earliness and grain yield, Giza-178 x Sakha-101; for plant height, and Sakha-106 x Giza-177; for chlorophyll content.

El-Badawy *et al*., (2022) estimated mid-parent and better-parent heterosis from fifteen crosses for five attributes in rice and found that two crosses, namely IET1444 x G 182 and NP856-9 x G 182 exhibited the highest significant and positive values for grain yield, respectively.

El-Gammaal *et al*., (2022) studied heterosis for twelve traits in rice including yield and quality traits in eighteen crosses of rice. They found that the most beneficial mid-parent and better-parent heterosis were obtained by the crosses Sakha 106 x Hispagran and GZ 10101-5 x Sakha; for No. of panicle plant-1, Sakha 107 x M 206 and Sakha 108 x M 206; for 1000 grain weight, Sakah 105 x M 206 and Sakha 108 x M 206; for grain yield, GZ 10101-5 x Hispagran and Sakha 108 x Hispagran; for hulling %.

Shrivastav *et al*., (2022) evaluated heterosis for eighteen attributes by crossing between 21 lines and three testers in rice. For grain production and other attributes. There was a significant estimation of better-parent and relative increase in both positive and negative directions. Five F1s showed strong heterotic potential for yield contributing characteristics and grain yield over CSR 43 (SV2) and Jaya (SV1).

Neupane (2022) estimated heterosis for eight traits of rice using 3 sets of crosses in L x T mating design for each set. For fertile grain number, one cross had significant and positive heterobeltiosis (Khumal -8 X Sukhadhan-2) and mid parent heterosis (IR775-39-80-2-2-2 X Khumal-4). When taking heterobeltiosis into account, no cross showed a significant heterosis value for thousand-grain weight. Five crosses, however, exhibited mid-parent heterosis values that were substantial.

Sunny *et al*., (2022) studied heterosis in twenty-one crosses of rice and found that three crosses exhibited significantly negative mid-parent heterosis, while one cross expressed significant heterosis relative to mid and better parent for plant height. Significantly positive heterosis relative to mid-parent for grain yield was detected for seven crosses. Moreover, the cross Baskots x Dehradun Pahari exhibited the best mid-parent heterotic effect for yield being 70.27%.

Das *et al*., (2023) estimated both types of heterosis (mid-parent and better-parent) for grain yield from fifty-five **crosses** of rice and found highly significant mid-parent and better-parent heterosis in three crosses, namely, Aruna x Varsha, Jyothi x Pavizham and Bharathy x Annapoorna.

Kushal *et al*., (2023) exploited three types of heterosis in 32 crosses including relative heterosis (mid-parent), heterobeltiosis (better-parent) and standard heterosis (over standard checks). They obtained three crosses with better values of standard heterosis over the two checks for days to 50% flowering. One cross (KNM 12469 X WGL 1119) exhibited significant and negative standard heterosis for plant height. Regarding plant yield, the most applicable standard heterosis was detected for the cross KNM 12469/Aganni. For hulling%, one cross expressed desirable standard heterosis values. None of the studied crosses expressed significantly positive heterobeltiosis or standard heterosis for milling%.

El-Naem *et al*. (2024) estimated heterosis for some important traits in fifteen crosses in rice. The crosses IR-12 G321 x Giza 178, 11-L236 x GZ-1368-S-5-4, IR-12 G 3213 x Nerica -7, IR 6500-127 x GZ 1368-S-5-4, IR 6500-127 x Giza 178, and crosses11 L 236 x Nerica-7, exhibited the best mid-parent heterosis for days to 50%, plant height, grain yield/ plant, grain shape, and milling % respectively.

Somtochukwu and Abiodun (2024) investigated mid-parent and better-parent heterosis for ten agronomic traits in rice and found that mid-parent heterosis for plant height ranged from -18.77 to - 59.83%, while better-parent heterosis ranged from -60.38 to +9.28% for. Moreover, the highest heterotic value was detected for the cross UPIA-2 x UPN-234 for this trait. Regarding grain yield, the ranges of mid-parent and better parent heterosis were from 214.54 to -83.05 and from -86.25 to 197.60, respectively. Moreover, the cross UPIA-2 x 234 exhibited the most desirable heterosis for grain yield.

Singh *et al.*, (2025) estimated heterosis for eleven traits in rice and found that the two crosses MTU1197 x BLM-9 and PKV-HMT x BLM-9 gave notable mid-parent heterosis for earliness. For plant height, one cross (R853-105-1-82-1 x ISM) expressed the best mid-parent heterosis, being 25.90%. The top cross RFS2019-1 X ISM elucidated a desirable better-parent heterosis of 15.15%.

Maneesha *et al* (2025) used L × T mating design to assess the heterotic effects over mid, better and standard parent for grain yield, head rice recovery and other traits. For flowering, plant height, number of filled grains per panicle, grain yield and kernel length five hybrids were high and significant relative heterosis, heterobeltiosis and standard heterosis. 12 hybrids showed significant positive over mid parent and three hybrids over better parent for 1000 grain weight.

2.3. Quality characteristics.

Waza *et al*., (2015) assessed gene action for rice yield using line x tester design with three males and six females. Their results showed that one parent had significant and positive GCA effects, moreover, one cross evinced the best SCA effects for yield attributable traits.

Menaka and Ibrahim (2016) estimated gene action for thirteen quality traits using the L x T mating approach, where eight lines were crossed with six testers. Two lines, namely, the ASD-16 line and Pusa Basmati-1 and one tester (Basmati 370), were explicitly the best general combiners for quality traits. Moreover, five crosses exhibited the most applicable specific combiners for quality traits.

Mohamed *et al*., (2016) studied the performance and gene action of thirteen quality traits in rice and found that non-additive type action was responsible for the behavior of these traits. Also, one parent, viz. Pant Sugandh Dhan-17 was the best general combiner for most quality traits. Concerning SCA effects, most crosses exhibited desirable values for quality traits.

Babu and Sreelakshmi (2018) assessed the combining ability of fourteen quality traits in twenty-one crosses of rice. They observed the preponderance of dominance and epistasis variance in controlling most quality traits. The most beneficial GCA effects for quality traits were detected for the parent Swarnamukhl followed by Bharani then NLR-33637. The best specific combiners were IR-164 x Swarnamukhi for kernel L/B ratio, Erramallelu x IR-72 for hulling %, IR-72 x Bharani for milling %, Erramellelu x Samba-Mahsuri for head rice recovery, PR-164 x Bharani for GT score.

Lingaiah *et al*., (2019) conducted an experiment to estimate gene action of nine cooking quality parameters. They found that the magnitude of dominance and epistasis was much higher than the additive effect for most quality traits. The best general combiners were MTU 1010 for hulling and milling %, WGL-23985 for kernel elongation and NH-686 for head rice recovery and kernel breadth. The best specific combiners for most quality attributes were spotted for the crosses WGL32100 x RP-Bio-5478-185, Ramappa x RP-Bio-5478-176 and Ramappa x RP-Bio 5478-185.

Renuka *et al*., (2019) studied L x T analysis using seven lines and four testers to assess combining ability for six quality traits in rice. Results elucidated the importance of non-additive genetic component in the inheritance of the six studied quality traits, namely, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth and Kernel L/B. One parent (RNR-15048) exhibited the best GCA effects for grain L/B ratio and kernel length, while tester IR-64 was the best combiner for kernel length and kernel L/B ratio. For all quality traits, two crosses viz, RNR 15048 / ADT 43 and MTU 1010 / IR 64 were of great value for rice breeders since they were very beneficial specific combiners.

Aamer and Ibrahim (2020) studied combining ability in fifteen crosses for six quality traits in rice. They found that variance due to GCA was more important than SCA for four crosses out of six. Two parents (Giza 178 and Giza 179) possessed meaningful GCA effects for five traits. Seven crosses exhibited the best SCA effects for yield and some other traits. Moreover, the best GCA were detected for milling in two parents (Sakha 105 & Giza 178), for head rice in two crosses (Giza 178 & WAB880 SG). Significantly positive SCA effects were observed for hulling%, milling% and head rice% in two crosses each.

Buelah *et al*., (2020) used L x T mating design to evaluate the combining ability of ten quality traits where four males were crossed to six females to generate forty crosses in rice. Analysis of variance revealed that GCA was more important than SCA for five quality attributes, namely, hulling%, kernel length, amylose content, gel consistency and alkali spreading value. However, the SCA component was more important for the other five quality traits (milling%, head rice recovery, kernel breadth, L/B ratio and gelatinization temperature). Five parents expressed their ability as good general combiners for most traits.

Moreover, four crosses were superior since they had the best SCA effects for most quality traits.

Kumar *et al*., (2021) studied the gene action of nine quality traits of forty-eight crosses resulting from L x T matting fashion where 4 lines were crossed with 12 testers. Dominance and epistasis were predominant for all attributes. Four testers and two lines performed well for GCA performance, and three crosses exhibited significantly positive SCA effects for most quality traits.

El-Gammaal *et al*., (2022) estimated both types of the combining ability of six quality traits through L x T mating approach with six lines and three testers. For hulling%, two parents (Sakha 107 & M206) along with two crosses ranked the first in their performance. Concerning, head rice (%), grain thickness and grain shape, the genotypes Sakha 107 and tester M 206 gave the best mean values. The magnitude δ^2 SCA was greater than δ^2 GCA for the five studied quality traits. This means that dominance and epistasis were predominant for such traits. Desirable GCA effects were obtained for parents Sakha 107, for hulling%, Sakha 108 for milling%, and Sakha 106 for head rice consistency. Beneficial SCA effects were detected by the crosses Sakha 105 x Hispagran for hulling%, Giza 177 x M206 for head rice recovery, Sakha 107 x Super-300 and GZ101015 x Hispagran for grain shape.

Shrivastav *et al*., (2022) evaluated combining ability for quality traits in rice using 89 genotypes (21 females x 3 males plus the parents and two checks). They found great variability among studied genotypes for quality traits. Variances due to SCA were higher than GCA for most studied attributes. Ten, eight, and four parents exhibited the best GCA effects for L/B ratio.

Kushal et al., (2023) used L x T mating design with eight lines and four testers to evaluate combining ability of six quality traits in rice. Results asserted significant differences for lines, testers and their crosses for all quality traits. The ratio GCA/ SCA clarified that dominance and epistasis were prevailing for hulling%, Milling%, head rice recovery kernel length, and kernel breadth. However, for kernel L/B ratio, the effects of GCA were more important than SCA. The line KNM-13568 was considered the best combiners for milling%, head rice recovery, kernel length, and kernel L/B ration. The cross KNM 14985x Agann exhibited the best SCA for hulling%, and head rice recovery.

Kumar and Pandy (2023) determined the gene action for three quality traits of rice using ten lines and three testers in line x tester pattern. Data revealed that the dominant genetic component was more important than the additive one for the three characters studied. Four lines and three crosses exhibited the most applicable effects for GCA and SCA, respectively for all traits.

El-Naem *et al*. (2024) studied the inheritance of five quality traits in line x tester model with five lines and three testers. They mentioned that the genotypes studied had apparent variations for all studied traits. Both types of genetic components (additive and non-additive) were responsible for the inheritance of all quality attributes except grain shape. The parent Giza 178 exhibited desirable GCA effects for most quality traits. Moreover, five crosses expressed desirable SCA for most quality traits.

Lingaiah *et al*. (2024) investigated the nature of gene action controlling the four quality traits of rice. Their results showed that the magnitude of specific combining ability was higher than the general one, revealing the prominence of dominance and epistasis for all quality traits. Three parents showed significant and positive GCA effects.

Santhiya *et al*., (2024) used L x T mating approach to elucidate the combining ability for ten quality traits in rice. They found that the non-additive component was predominant for most quality traits. Also, one parental line and two testers proved to be good combiners for quality traits. Regarding SCA, two crosses, namely, CO-55 × IC-457996 and ADT-54 × IC-115439 exhibited practical value for quality characteristics in rice.

Thang (2024) gained information about gene action controlling six quality traits from fifteen crosses resulting from crossing five males and three testers. The magnitude of SCA's variance was greater than that of GCA for all quality traits, illuminating the importance of non-additive genetic variance in governing the traits studied. One parent (C70) appeared to be the best combiner for head rice recovery.

Mohanty *et al* (2025) studied gene action for grain quality traits by using line ×tester. The results indicated dominance variance was greater than additive variance, showing that influence of non-additive gene effects on trait inheritance.

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The present study was carried out at Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt, during 2023and 2024 rice growing seasons and the quality traits were studied at the Rice Technology and Training Center (RTTC), Alexandria, Egypt.

Experimental Materials

The plant materials of the present work involved ten parents, six of them represented the male parents, i.e. Sakha104, Sakha106, GZ11332, Sakha108, Sakha109, Sakha101 and 4 testers Viz., IHL17, IHL65, IHL175, Super303 of Oryza sativa. The names, pedigree, origin and type of parents are presented in Table (1)

Table 1: Names, pedigree, and type of selected rice parent.

NO	**Name**	**Pedigree**	**Origin**	**Type**
1	Sakah104	GZ4096-8-1/GZ4100-9	Egypt	Japonica
2	Sakha 106	(Giza 177 / Hexi 30)	Egypt	Japonica
3	Sakha 101	(Giza 176 / Milyang 79)	Egypt	Japonica
4	GZ11332	GZ 8455-9-1-1-2/ SKC 23819HUA 565	Egypt	Japonica
5	Sakha 108	(Sakha101/ HR5824-B-3-2-3// Sakha 101)	Egypt	Japonica
6	Sakha 109	Sakha 105 x Sakha 101	Egypt	Japonica
7	IHL17	Unknow	IRRI	Japonica
8	IHL65	Unknow	IRRI	Japonica
9	IHL175	Unknow .	IRRI	Japonica
10	SR303	Unknow	Egypt	Japonica

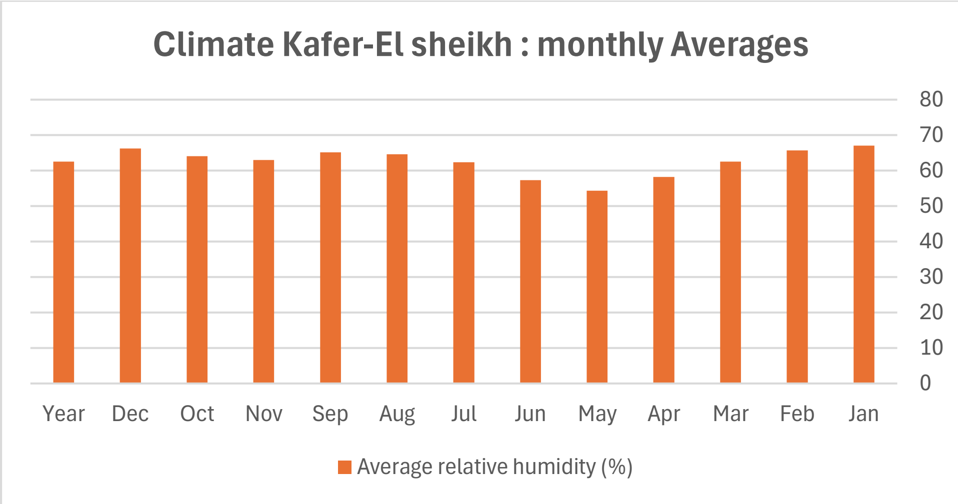
3.2 Experimental Site:

According to a previously described method, soil chemical and physical properties, as well as soil texture of the 0–30-cm deep soil, were measured in the experimental field across two rice growth seasons 2023 and 2024 according to Black et al., 1965 and presented in Table 2. The average monthly relative humidity during the 2024 season in Kafer-El sheikh is shown on Fig.1.

Table 2: Physical and Chemical Properties of the Soil expermient

Characters	2023	2024
Particle size distribution		
Sand %	11.69	11.30
Clay %	53.57	54.15
Silt %	32.35	32.15
Texture	Clay	Clay
Organic matter %	1.39	1.40
Chemical analysis		
pH (1:2.5)	8.25	8.35
EC (ds.m-1)	0.7	0.68
Available N (ppm)	15.85	17.70
Available P (ppm)	15.09	14.0
Available K (ppm)	248.85	236.31
Anions (Cmolc/ kg soil)		
CO_3^{--}	--	--
HCO_3^-	5.60	5.65
Cl^-	9.64	9.54
SO_4^{--}	16.89	18.04
Cations (Cmolc/ kg soil)		
Ca	11.19	11.65
Mg	4.60	4.95
Na	1.58	1.90
K	14.35	15.87

Fig.1: The average monthly relative humidity during the 2024 season in Kafer- El sheikh.



Source: The Global Historical Weather and Climate Data in 2024.

3.3 Field experiment

- **In the first season**
- These materials were planted during 2023 season in three successive dates of planting with ten days intervals in order to overcome the differences in flowering time among the Lines and the Testers to get good synchronization to make the crosses among the parental lines to obtain the hybrid seed. Thirty-day old seedlings of each parent were individually transplanted in the permanent field in ten rows. Each row was 5 m long and contained 25 hills. At flowering time, the six lines were crossed with the four testers excluding reciprocals through line × tester mating design to produce 24 F_1 hybrids. Bulk emasculation was conducted using hot-water technique by **Butany (1961).**

B. The second season:

In 2024 season, the seeds of parents and their F1 hybrids were sown in dry seedbed and 30 days after sowing, the seedlings of 34 produced rice genotypes (6Lines, 4Testers and 24 F1's) were transplanted in randomized complete block design (RCBD) with three replications. Each replicate comprised of 5 rows of each genotype. The row was 5 m long and 20x20 cm a part was maintained between rows and seedlings. Single seedlings were planted on each hill. Observations were recorded on randomly selected ten plants for each parent and F1 generation for each replication as recommended by **IRRI (2018).**

In the two seasons, recommended package of practices and plant protection measures such as field preparation, transplanting, fertilizers, weed controls… etc., were followed as recommended by **RRTC (2023).**

3.4 Data recorded

The data were recorded according to Standard Evaluation System (SES) of **IRRI (2018),** for all studied traits as given below.

3.4.1. Morphophysiological traits:

- **Days to 50% heading**: It was determined as the number of days from sowing date to 50% heading.
- **Plant height (Cm):** was determined as length of the main stem measured from soil surface to the tip of the main panicle.
- Number of tillers plant-1: measured by counting the total number of tillers plant-1 before harvest.
- **Flag Leaf Area (cm2):** determined by measuring length and width main stem flag leaf x 0.75.
- **Flag Leaf angle (o):** that is the angle between the stem of the panicle and flag leaf.
- **Chlorophyll content (SPAD)**: determined according to the method

described by **Lichtenthaler and Buschmann (2001).**

3.4.2. Yield and its component traits:

- **Number of panicles per plant^{-1}:** counted by the number of fecundated tillers per plant, only panicles in the full ripe stage counted.
- **Panicle length (cm) :** Determined as the length of main panicle, measured from panicle base up to apiculus of the upper most spikelet of the panicle.
- **Panicle weight (g):** Determined as the weight of the main panicles of the plant.
- **spikelet's fertility per panicle (%):** The fertile spikelet's were identified by pressing the spikelet's with the fingers and counting those which had grains and were calculated as follows: .

$$\text{Spikelet's fertility (\%)} = \frac{\text{No. of fertile spikelet's /panicle}}{\text{No. of all spikelet's per panicle}} \times 100$$

- **Weight of 1000 grains** (g): It was recorded as the weight of 1000 random filled grains of each plant.
- **Grain Yield per plant (g):** Determined as the weight of each individual grain yield / plant.
- **Harvest index (HI %):** Measured by the next formula:

$$\text{Harvest Index (\%)} = \frac{\text{Gran yield or Economic yield(g)/ plant}}{\text{Biological yield (g) / plant}} \times 100$$

This formula was suggested **by Donald and Hamblin (1976), and Aidy *et al.*, (1992).**

3.4.3. Grain quality traits.

1. Hulling percentage (Brown rice recovery or Kargo rice): Using a huller machine (Satake) in the grain lab of the Rice Technology and Training Centre, 150 g of cleaned rough rice samples with 12–14% moisture content of were measured. paddy rice was de-husked to obtain brown rice. According to Ghosh et al. (1971), the hulling % was computed as follows:

$$\textbf{Hulling \%} = \frac{\textbf{Total brown rice weight(g)}}{\textbf{Total rough rice weight (g)}} \times 100$$

2. Milling percentage: Brown rice was consequently milled using Mc Gill Miller No.2 (Whitener) to obtain the white rice (milling yield). The sample was milled for 60 sec. The milled rice sample was collected, and the weight was taken. **Ghosh *et al.* (1971)** was determined milling percentage as follows:

$$\textbf{Milling \%} = \frac{\textbf{Total milled rice weight(g)}}{\textbf{Total weight of rough rice (g)}} \times 100$$

3. Head rice percentage: Using a rice-sizing apparatus, whole grains (head rice) were segregated based on broken size (less than ¼th of grain length) before being weighed. The head rice percentage was determined by**:**

$$\textbf{Head rice \%} = \frac{\textbf{Total weight of head rice (g)}}{\textbf{Total rough rice weight (g)}} \times 100$$

4. **Grain shape**: Grain dimensions (length and width) were taken on 15 normal grains from each plant with the help of a micrometer. Length /width ratio (grain shape) was calculated from these values as follows:

$$\textbf{Grain shape \%} = \frac{\textbf{Grain length (mm)}}{\textbf{Grain width(mm)}} \times 100$$

The following scale as suggested **by Juliano 1993 was used to describe the grain shape (Table 4).**

Table (3): Description of the grain shape.

a) shape	b) Length / width ratio
Slender	**Over 3.0**
Medium	**2.1 to 3.0**
Bold	**1.1 to 2.0**
Round	**1.0 or less**

3.5. Statistical analysis:

3.5.1. Analysis of variance

Standard statistical analysis was done for all traits to test the significance of all genotypes (**Steel and Torrie, 1980).** When differences among entries were found significant, L x T analysis was adopted according to the approach of **Kempthorne (1957)** as in **Table 4.**

Table (4): Analysis of variance and the expectations of mean squares (E.M.S) for top crosses in rice.

Source of variation	d.f	M.S	EMS
Replications	**r-1**		
Genotypes	**g-1**		**(σ2e+ r σ2g)**
Parents	**p-1**		**(σ2e + rσ2p)**
Crosses	**c-1**	**Mc**	**(σ2e + rσ2c)**
Parents vs. Crosses	**1**		**(σ2e + r σ2p.v.sc.)**
Lines	**L-1**	**ML**	**(σ2e + rσ2lt +**
Testers	**t-1**	**Mt**	**rtσ2L)**
L x T	**(L-1) (t-1)**	**MLxt**	**(σ2e + rσ2lt + rl σ2t)**
Error	**(r-1) (g-1)**	**Me**	**(σ2e + rσ2lt)**
			σ2e

Where:

r = number of replications.

G = number of genotypes.

P = number of parents.

C = number of crosses.

L = number of lines.

T= number of testers.

M_c = Crosses mean squares.

M_L = Lines mean squares (G.C.A mean square).

M_t = Testers mean squares (G.C.A mean square).

M_{Lxt} = Lines x testers mean squares (S.C.A mean square).

M_e = Error mean squar

3.5.2. Estimation of variance components

The following equations were used to estimate both types of combining abilities as follows:

$$\sigma 2gi = \sigma 2gcai = \frac{M_L - M_{LT}}{r\ x\ t}$$

$$\sigma 2gj = \sigma 2gcaj = \frac{M_L - M_{LT}}{r\ x\ l}$$

$$\sigma 2Sij = \sigma 2scaij = \frac{M_{LT} - M_E}{r}$$

Variances due to general and specific combining abilities were computed as follows:

$$\sigma 2gca = \text{Cov. (H.S.)} = \frac{M_L + M_T + 2M_{LT}}{r\ (L + t)}$$

$$\sigma 2sca = \text{Cov. (F.S.)- Cov. (H.S.)} = \frac{M_{LT} + M_E}{r}$$

Where,

Cov. (H.S.) = covariance between half sibs,

Cov. (F.S.)= covariance between full sibs.

3.5.3. Estimation of general combining ability (GCA) and specific combining ability (SCA) effects:

Analysis of variance was performed for morphophysiological, yield and quality traits. Then, the genotypes mean squares were further partitioned to both types of combining ability. The approach used to analyse GCA and SCA effects of the Xijk as given by **Kempthorne (1957) was as follows:**

Xijk = μ + ĝi + ĝj + ŝij + eijk

Where:

Xijk= The value of cross between one parent (i) and another parent (j).

μ =overall population mean

ĝi = GCA effect of the i the male parent (tester).

ĝj = GCA effect of the j the female parent (line).

ŝij = SCA effect of is the cross combination.

eijk = the error associated with the Xijk observation.

I = number of male parent (tester) = 1, 2, …m.

J = number of female parent (line) = 1, 2, …f

K = number or replication = 1, 2, … r

The individual effects were estimated as follows:

- **GCA for lines:**

$$\hat{g}i = \frac{X_{i..}}{tr} - \frac{X_{...}}{Itr}$$

Where:

Xi… = total of all i the female (line) parent over all male parents (testers) and replications.

X… = total of all females (line) over all males (testers) and replications.

- **GCA for testers:**

$$\hat{g}_t = \frac{X_{t..}}{lr} - \frac{X_{...}}{ltr}$$

Where:

Xt… = total of the t the male (tester) parent over all females (lines) and replications.

I = number of Lines

t = number of testers, r = number of replications

- **Specific combining ability effects:**

$$\hat{s}ij = \frac{XIt}{r} - \frac{XI}{tr} - \frac{Xt}{Ir} + \frac{X\ldots}{Itr}$$

Where:

Xit = total of the it the hybrid combination over all replications.

(d) **Stander error for combining ability effects**:

S.E. (GCA for lines) = $\sqrt{(Me/rt)}$

S.E. (GCA for testers) = $\sqrt{(Me/rI)}$

S.E. (SCA effects) = $\sqrt{(Me/r)}$

S.E. (ĝi-ĝj) line = $\sqrt{(2Me/rt)}$

S.E. (ĝi-ĝj) tester = $\sqrt{(2Me/rl)}$

S.E. (ŝij –ŝkl) = $\sqrt{(2Me/r)}$

3.5.4. Heterosis:

There are two formulas usually used for estimation of heterosis are as follows:

1. Heterosis is relative to mid-parents (MP).
2. Heterosis is relative to better parent (BP).

We used two formulas of heterosis in this study as follows:

- **Heterosis relative to mid-parents % (MP):**

The deviation of the F1 hybrid's mean over the average of its two parents was used to calculate the amount of heterosis suggested by Mather (1949) and Mather and Jinkes (1982) as follows:

$$MP\% = \frac{\bar{F}_1 - MP}{MP} \times 100$$

To test the significance of heterosis for the above case, L.S.D values according to Steel and Torrie (1980) by using the following formula

LSD for MP = $t_{0.01}^{0.05}\sqrt{\frac{3EMS}{2R}}$

2. Heterosis relative to better parent % (BP):

$$BP\% = \frac{\overline{F}_1 - B.\overline{P}}{B\overline{P}} \times 100$$

The better parent for any character is that having the higher mean value, except for heading date, plant height and flag angle, where the better parent is the one with the lower mean value.

LSD for better parent =

$$t_{0.01}^{0.05}\sqrt{\frac{2EMS}{r}}$$

RESULTS
And
DISCUSSION

4.RESULTS AND DISCUSSION

For simplicity, the results of this work regarding analysis of variance, mean performance, combining ability and heterosis for all traits studied will be presented and discussed under the following topics.

4.1. Analysis of variance and mean performance:

4.1.1.A. Analysis of variance morphophysiological traits:

Data presented in Table 5 showed Mean squares estimates for the ordinary and combining ability analyses for morphophysiological traits.

The mean squares of genotypes and their portions; parents, crosses and parents vs. crosses were highly significant for all studied Morphophysiological traits except those of testers for No. of tillers plant-1. The variations among crosses were partitioned into lines, testers and line × tester. Highly significant differences were detected among such partitions for most attributes, indicating the wide diversity and genetic diversity among the germplasm utilized in the study. Parent vs. crosses mean squares as an indicator to the heterosis overall crosses, were found to be highly significant for the studied morphophysiological, indicated that average heterosis were significant or highly significant for the studied traits.

The comparative estimates of general (σ^2GCA) and specific combining ability (σ^2SCA) variances showed that the value of the σ^2GCA variance was less than the value of σ^2SCA variance. This finding indicates that the non-additive type of gene action was of greater importance in the inheritance of these traits. It suggested greater importance of non-additive gene action in their expression and indicated very good prospects for the exploitation of non-additive genetic variation for all morphophysiological traits through hybrid rice. Similar results were reported by **El-Gammal et al., (2022), Kushal et al. (2023), Das et al., (2023), Abo-Yousef et al., (2024); and El-Naem et al., (2024).**

Table (5): Mean square of some morphophysiological traits of rice.

S.O. V	DF	Days to 50% heading (days)	Plant height (cm)	No. of tillers / plant	Flag leaf area(cm2)	Flag leaf angle(°)	Chlorophyll content (SPAD)
Reps	2	6.48	0.64	0.03	1.62	1.17	1.97
Entries	33	232.81 **	78.48 **	20.72 **	77.94 **	133.28 **	31.67 **
Parents	9	262.30 **	85.72 **	19.50 **	10.98 **	135.29 **	32.74 **
Crosses	23	174.05 **	33.72 **	11.48 **	57.64 **	73.93 **	12.84 **
P vs C	1	1318.84 **	1042.80 **	244.40 **	147.60 **	1480.26 **	455.20 **
Lines	5	380.36 **	91.13 **	23.78 **	50.86 **	150.67 **	19.94 **
Testers	3	151.27 **	46.37 **	0.68	231.21 **	15.15 **	21.98 **
Line x Tester	15	109.84 **	12.05 **	9.54 **	25.19 **	60.11 **	8.65 **
Error	66	2.73	1.34	0.64	2.16	0.60	2.05
σ2GCA		1.62	0.55	0.05	0.82	0.35	0.11
σ2SCA		35.70	3.57	2.97	7.68	19.84	2.20
σ2 GCA/σ2 SCA		0.05	0.154	0.017	0.107	0.017	0.05

The non additive components were predominant where, the σ2GCA/σ2 SCA ratio was less than unity for days to 50%heading, plant height, No. of tillers/plant, flag leaf area and angle, as well as, chlorophyll content ,that mean, to develop new recombination should be delay the selection to late generation, these results were confirmed with **sunny., et al (2022)** found the GCA/SCA ratio was less than unity demonstrating the importance of non-additive gene action for all characters.

4.1.1.B. Mean performance for morphophysiological traits

The mean performance of all attributes was presented in Table 6. For days to 50% heading, the parent Sakha106 exhibited the lowest mean value being 88.67 cm, while the tester Super303 gave the best mean value as compared to other studied parents. Whereas the cross Sakha108xIHL65 expressed the most desirable effects for days to 50% heading recording 81.00 days **(Table 6).**

Regarding plant height, data in Table 6. Showed that the cross Sakha101xSuper303 (95.33 cm) was the best among all crosses since it had the lowest significant mean value for this trait followed by the cross Sakha101x IHL175 (98.94 cm). On the other hand, the cross Sakha104xIHL175 was the tallest genotype for plant height, with a mean value of 110.00 cm.

For number of tillers plant-1, The most desirable mean value was detected for the cross Sakha109xSuper303 (32.67) followed by the cross Sakha109xIHL17 (30.33) then the cross Sakha108xSuper303 (29.00) (Table 6).

Regarding flag leaf area, the parents IHL65, IHL 175 and Sakha 104 recorded the highest mean values (36.33, 36.00 and 36.00 cm) respectively. The crosses Sakha 109xSuper303 and GZ11332xSuper303 recorded the highest desirable mean performance for flag leaf rea (48.67and 48.00 cm) respectively. In contrast the lowest mean performance undesirable was Sk101xIHL65 cross (33.72cm) and GZ11332xIHL75 (35.40cm).

In addition to, flag leaf angle and chlorophyll content, the cross Sakha109xSuper303 exhibited the most desirable mean value being 45.33 and 47.67, respectively (Table 6). Also, the two crosses Sakha104xSuper303 (45.06) and Sakha109xIHL17 (46.17) ranked the best second for the two respective **traits (Table 6).**

Table (6): Mean performance of some morphophysiological traits in rice.

Genotype	Days to 50% heading(days)	Plant height (cm)	No. of tillers / plant	Flag leaf area	Flag leaf angle	Chlorophyll content
Sakha104	107.33	106.00	27.67	36.00	35.33	39.33
Sakha106	88.67	103.00	22.67	32.33	37.00	39.62
GZ11332	89.33	100.67	20.33	34.67	26.33	40.67
Sakha101	89.33	95.00	24.33	32.00	18.33	43.02
Sakha108	103.67	100.00	26.00	31.00	30.67	31.00
Sakha109	92.67	102.33	22.67	33.33	18.33	36.81
IHL17	110.33	96.00	25.33	34.67	20.67	39.67
IHL65	110.67	88.33	22.67	36.33	25.33	35.76
IHL175	102.67	92.33	20.33	36.00	31.67	38.62
Super303	89.67	98.00	26.67	35.67	30.00	40.29
Sakha104x IHL17	81.67	109.00	28.67	42.50	35.82	44.15
Sakha104x IHL65	83.67	109.00	28.33	40.70	39.99	44.33
Sakha104x IHL175	82.67	110.00	26.67	41.04	36.67	39.76
Sakha104xSuper303	87.33	102.67	28.00	47.31	45.06	43.70
Sakha106x IHL17	89.67	107.67	25.67	39.00	35.27	44.21
Sakha106x HL65	91.00	106.67	25.67	39.70	32.29	41.80
Sakha106x IHL175	85.67	108.00	27.67	39.67	39.33	40.07
Sakha106xSuper303	90.67	109.00	21.33	46.53	38.63	42.54
GZ11332x IHL17	90.00	104.00	25.67	40.21	40.33	45.06
GZ11332x IHL65	89.33	105.00	27.33	34.41	31.67	42.75
GZ11332x IHL175	85.67	104.33	26.33	35.40	31.33	45.18
GZ11332xSuper303	87.67	103.00	27.00	48.00	26.33	45.05
Sakha101x IHL17	90.67	103.27	27.33	35.63	31.00	41.93
Sakha101x IHL65	99.33	104.17	26.67	33.72	35.33	41.20
Sk101x IHL175	111.67	98.94	25.67	38.48	33.00	39.36
Sakha101xSR303	100.67	95.33	25.00	47.33	26.33	42.18
Sakha108x IHL17	85.33	106.53	26.33	40.62	34.33	42.73
Sakha108x IHL65	81.00	106.00	27.67	44.20	30.33	43.77
Sakha108x IHL175	100.33	108.00	25.00	45.40	34.99	44.37
Sakha108xSR303	89.67	104.00	29.00	42.93	39.31	43.33
Sakha109x IHL17	90.00	105.00	30.33	45.67	39.77	46.17
Sakha109x IHL65	95.67	105.20	27.33	39.42	39.00	40.37
Sakha109x IHL175	102.00	106.97	28.00	40.92	36.00	43.07
SakhaK109xSuper303	81.67	102.67	32.67	48.67	45.33	47.67
Overall mean	92.86	103.12	26.26	39.40	33.27	41.75
LSD 5%	2.70	1.88	1.30	2.40	1.26	2.33
LSD 1%	3.58	2.50	1.73	3.18	1.67	3.10

4.1.2. Yield and its related traits

4.1.2.A Analysis of variance for yield and its related traits

Data **in Table (7**) displayed the mean squares of seven yield traits viz, No. of panicle plant-1, panicle length, panicle weight, spikelet fertility, 1000 grain weight, grain yield plant-1, and harvest index. Genotypes and their portions; parents, crosses and parents vs. crosses were highly significant for all studied yield and its components traits in mean square value. The variations among crosses were partitioned into lines, testers and line × tester. For most attributes highly significant differences were detected among such partitions, emphasizing that the wide diversity and genetic diversity among the germplasm utilized in the study. Parent vs. crosses mean squares as an indicator to the heterosis overall crosses, For the studied grain yield and its components were found to be highly significant, indicated that average heterosis were significant or highly significant for the studied traits.

The variances (σ^2GCA) and specific combining ability (σ^2SCA) showed that the value of the σ^2GCA variance was less than the value of σ^2SCA variance. This finding indicates that the non-additive type of gene action governed the inheritance of these traits. It showed greater importance of non-additive gene action in their expression. Such variability for rice grain yield and its contributing traits was investigated **by many scientists, such as Gaballah et al., (2021), Ayuba et al., (2022), Bayoumi et al., (2022), Das et al., (2023), Abo-Yousef et al., (2024), El-Naem et al., (2024), Kummar et al., (2024), Modarries et al., (2024) and Vennila (2024).**

For σ^2GCA /σ^2SCA ratio was less than unity for all the yield and its components, indicated to the important role for non-additive gene action in the genetic control for these characters, these results were confirmed with GCA and **SCA values.**

Table (7): Mean square of yield and its components in rice.

S.O. V	DF	No. of panicles/ plant	Panicle length (cm)	Panicle weight (g)	Spikelet fertility	1000 grain weight (g)	Grain yield/ plant (g)	Harvest index %
Reps	2	0.16	0.20	0.05	0.17	1.07	0.81	1.11
Entries	33	20.21 **	5.83 **	1.09 **	19.33 **	8.90 **	66.51 **	84.92 **
Parents	9	17.27 **	3.87 **	0.71 **	33.65 **	7.79 **	20.55 **	73.30 **
Crosses	23	11.28 **	4.95 **	0.90 **	3.81 **	5.26 **	57.41 **	56.24 **
P vs C	1	252.05 **	43.64 **	8.87 **	247.34 **	102.68 **	689.61 **	849.19 **
Lines	5	26.23 **	8.11 **	1.35 **	3.72 **	15.07 **	124.15 **	142.28 **
Testers	3	7.02 **	8.51 **	2.96 **	5.65 **	3.41 **	103.51 **	17.75 **
Line x Tester	15	7.15 **	3.18 **	0.34 **	3.48 **	2.36 **	25.94 **	35.25 **
Error	66	0.45	0.06	0.02	0.42	0.59	0.95	1.03
σ^2GCA		0.10	0.04	0.01	0.01	0.07	0.79	0.53
σ^2SCA		2.23	1.04	0.11	1.02	0.59	8.33	11.41
σ^2GCA/ σ^2SCA		0.05	0.038	0.10	0.009	0.11	0.095	0.047

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

4.1.2.B. Mean performance for yield and its components:

Mean value for yield and its attributing traits are presented **in Table 8.** For the number of panicles plant-1, the top cross Sakha109xSuper303 was the best among all attributes since it expressed the highest significant mean value (31.00) for this trait compared with any other cross. Moreover, this cross (Sakha109xSuper303) was significantly higher than any other cross under study. For panicle length, the same previous cross (Sakha109xSuper303) produced the highest mean value for this trait being 28.52 cm followed by the cross Sakha109xIHL17 with a mean value of 27.54 cm.

Regarding panicle weight, the parental varieties Super303(5.05 g) and Sakha101 (4.79 g) obtained the highest mean performance for panicle weight. IHL175 (3.42 g) and IHL65 (3.77 g) gave the lowest value. While the crosses Sakha109xSuper303, Sakha109x IHL17 and Sakha104xSuper303 showed the highest desirable panicle weight among the other crosses. Their values were 5.77, 5.67 and 5.56 g respectively. The lowest values were recorded with GZ11332xIHL17 (3.78 g) and GZ11332xIHL175 (3.88 g).

The results indicated that Sakha101and Sakha109 parents revelated the highest mean performance for spikelet fertility. Their values were 95.99 and 95.27. The crosses Sakha109xSR303(98.36) and Sakha109xIHL17 (98.20) showed the highest value compared to other crosses. On the other hand, Sakha104xIHL65 was the lowest crosses. It recorded 93.71 mean performance followed by Sakha106xSuper303 (95.00). The parents Sakha104 (88.57) and Sakha106 (93.13) displayed the lowest value among other parents.

The top cross Sakha108xSuper303 exhibited the most desirable mean value for 1000 grain weight (32.60 g) followed by the cross Sakha109xSuper303 (32.53 g). However, the parent IHL65 (30.33 g) gave the best mean value for this trait but was still significantly lower than the best top cross Sakha109xSuper303. Conversely, the lowest value among parents were Sakha104 (25.37g), and Sakha106 (26.43g). The undesirable crosses were Sk104xIHL175 and Sk104xIHL17. Their mean performance recorded (28.38g and 28.60g) respectively **(Table 8).**

For grain yield plant-1, the cross Sakha109xSuper303 again expressed the highest positive and significant mean value as compared to any crosses, recording 52.27 g, followed by the cross Sakha108xSuper303 (48.51 g) and the cross Sakha109xIHL17 (48.82 g). Moreover, the tester IHL175 exhibited the highest mean value (41.17 g) for this trait as compared to other parents.

Concerning the harvest index, again, the cross Sakha109xSuper303 expressed the highest significant mean value, recording 58.43% as compared to other genotypes. Whereas the parent IHL175 was the best among all studied parents, giving a mean value of 46.27% **(Table 8).**

It could be concluded that the top cross Sakha109xSuper303 was the best among all studied genotypes since it exhibited the highest significant mean value of grain yield plant-1 and most of its related traits. This cross was prospective and could be used in a future rice breeding program.

Table (8): Mean performance of yield and its related traits in rice.

Genotype	No. of panicles/ plant	Panicle length (cm)	Panicle weight (g)	Spiklete fer- tility	1000 grain weight (g)	Grain yield/ plant (g)	Harvest in- dex %
Sakha104	24.00	26.08	4.59	88.57	25.37	36.53	42.00
Sakha106	21.33	24.87	4.15	93.13	26.43	35.73	47.51
GZ11332	18.67	23.33	4.03	94.29	30.03	36.86	43.37
Sakha101	23.00	25.24	4.79	95.99	27.53	39.66	42.83
Sakha108	24.00	25.08	4.06	95.05	28.33	33.67	33.67
Sakha109	19.67	23.05	4.42	95.27	28.96	35.19	32.96
IHL17	22.67	25.69	4.08	93.93	27.12	36.01	40.85
IHL65	19.67	23.28	3.77	93.46	30.33	34.33	44.51
IHL175	17.67	24.57	3.42	85.69	28.00	41.17	46.27
Super303	24.00	23.18	5.05	95.64	29.64	40.59	37.93
Sakha104x IHL17	25.67	26.50	4.77	95.48	28.60	37.97	42.48
Sakha104x IHL65	25.33	27.00	4.65	93.71	29.04	38.27	46.98
Sakha104x IHL175	24.67	26.21	4.82	97.24	28.38	41.51	47.40
Sakha104xSuper303	25.33	26.52	5.56	96.85	28.77	40.00	44.53
Sakha106x IHL17	24.33	25.50	4.52	95.51	29.80	36.32	48.99
Sakha106x HL65	25.00	23.52	4.70	96.27	30.83	37.43	48.80
Sakha106x IHL175	26.67	26.21	4.84	97.39	31.97	45.74	51.16
Sakha106xSuper303	24.33	23.70	5.55	95.00	30.03	42.33	47.63
GZ11332x IHL17	23.00	26.21	3.78	96.96	30.38	43.82	48.99
GZ11332x IHL65	22.67	25.35	4.63	96.00	31.67	43.24	47.10
GZ11332x IHL175	23.00	24.26	3.88	97.33	30.79	44.46	46.49
GZ11332xSuper303	23.67	25.61	4.93	97.14	31.50	45.05	43.93
Sakha101x IHL17	25.00	26.43	4.81	96.33	28.87	34.67	44.18
Sakha101x IHL65	24.00	23.60	3.95	97.20	30.03	40.18	44.37
Sakha101x IHL175	23.67	25.35	4.80	95.33	29.00	40.44	40.85
Sakha101xSuper303	22.67	26.20	5.48	97.24	30.20	43.59	43.29
Sakha108x IHL17	24.33	26.24	4.86	95.58	29.40	44.81	46.57
Sakha108x IHL65	24.67	25.80	4.75	96.43	30.53	44.37	44.83
Sakha108x IHL175	23.00	26.06	5.27	96.25	29.30	44.15	44.94
Sakha108xSuper303	27.33	27.44	5.50	97.78	32.60	48.51	54.21
Sakha109x IHL17	28.00	27.54	5.67	98.20	32.33	48.82	54.73
Sakha109x IHL65	24.00	24.20	4.47	95.28	30.50	38.11	45.42
Sakha109x IHL175	26.67	26.92	5.25	97.63	32.00	48.32	54.21
Sakha109xSuper303	31.00	28.52	5.77	98.36	32.53	52.27	58.43
Overall mean	23.90	25.45	4.69	95.51	29.73	41.00	45.66
LSD 5%	1.09	0.41	0.23	1.06	1.26	1.59	1.66
LSD 1%	1.45	0.55	0.30	1.41	1.67	2.11	2.20

4.1.3. Grain quality traits

4.1.3.A. Analysis of variance for grain quality traits:

Mean squares due to the four quality traits (hulling%, milling%, head rice recovery, and grain shape) is presented in Table 9. The mean squares of genotypes and their portions; parents, crosses and parents vs. crosses were highly significant for all studied grain quality traits. The variations among crosses were partitioned into lines, testers and line × tester. Highly significant differences were detected among such partitions for most attributes, indicating the wide diversity and enough genetic diversity among the germplasm utilized in the study. Parent vs. crosses mean squares as an indicator to the heterosis overall crosses, were found to be highly significant for the studied grain quality traits, indicated that average heterosis were significant or highly significant for the studied traits.

General (σ^2GCA) and specific combining ability (σ^2SCA) variances elucidated that the value of the σ^2GCA variance was less than the value of σ^2SCA variance. This finding indicates that the non-additive type of gene action was of adjustment in the inheritance of these traits. It demonstrated greater importance of non-additive gene action in their expression and indicated very good prospects for the exploitation of non-additive genetic variation for all quality traits. Comparable results were reported **by El-Gammaal et al., (2022), Shrivastav et al., (2022), and El-Naem et al., (2024).**

For σ^2GCA /σ^2SCA ratio was less than unity for the hulling, milling, head rice recovery and grain shape indicated the important role for non-additive gene action in the genetic control for these characters.

Table (9): Mean squares of some quality traits in rice.

S.O. V	DF	Hulling %	Milling %	Head rice recovery	Grain shape
Reps	2	0.41	0.05	0.13	0.023
Entries	33	4.18 **	4.26 **	73.43 **	0.273 **
Parents	9	2.66 **	4.11 **	116.25 **	0.100 **
Crosses	23	3.96 **	2.74 **	27.07 **	0.270 **
P vs C	1	22.86 **	40.58 **	754.43 **	1.904 **
Lines	5	3.59 **	3.21 **	67.86 **	0.219 **
Testers	3	6.43 **	5.30 **	34.62 **	0.455 **
Line x Tester	15	3.60 **	2.07 **	11.97 **	0.249 **
Error	66	0.42	0.17	0.05	0.008
σ^2GCA		0.01	0.02	0.38	0.001
σ^2SCA		1.06	0.64	3.97	0.08
σ^2GCA/ σ^2SCA		0.009	0.03	0.009	0.013

*** and ** significant at 0.05 and 0.01 levels of probability, respectively.**

4.1.3.B. Mean performance for grain quality traits:

Mean performance for all quality traits is presented in **Table 10**. For hulling%, the most desirable top cross was Sakha104xIHL65 (82.00%) followed by the cross Sakha106xSuper303 (81.58%). However, the best tester among all parents was IHL65 with a mean value of 80.50%.

With respect to milling shown in table 10 the highest value for milling were recorded of parents IHL65 and Sakha104 (72.70 and 71.80 %). The cross Sakha104xIHL65 (73.55%) and Sakha109xIHL175 (73.12%) exhibited the highest mean performance for milling trait. On the other hand, Sakha108 had the lowest mean performance among parents (68.25%). The cross Sakha106xSuper303 had the lowest mean performance among crosses (70.04%).

It is clear from the data that the parental lines Sakha 104 and Sakha106 had the highest value compared to other parents (70.30and 69.11%). In addition to the crosses Sk104xIHL175 and Sk106xIHL175 gave the highest values for head rice recovery compared to other crosses (75.71and 72.59%). In contrast, Sakha109 was the highest mean performance among parents (53.35%). The crosses Sakha108xIHL75 and Sakha101xSuper303 had the lowest value compared to other crosses. They were (62.28 and 63.08) respectively.

It could be noticed that the short to bold grain genotype was the most desirable grain shape. Among parents, the parental tester IHL17 was the lowest mean performance (1.53). The crosses Sakha 106xIHL65and GZ11332xIHL17 were the lowest values among crosses. The highest mean values were recorded by the parent IHL175and Sakha106 (2.04), While the highest value among crosses were recorded by GZ11332xSuper303 and Sakha101xSuper303 (2.85, 2.78 and 2.67) for grain shape. The results indicated the highest values in all genotypes were grain shape medium.

Table (10): Mean performance of quality traits in rice.

Genotype	Hulling %	Milling %	Head rice recovery	Grain shape
Sakha104	79.06	71.80	70.30	1.65
Sakha106	77.15	70.00	69.11	2.04
GZ11332	79.64	70.66	66.40	1.87
Sakha101	78.55	70.38	68.58	1.99
Sakha108	79.34	68.25	60.27	2.09
Sakha109	78.47	70.07	53.35	2.02
IHL17	79.68	70.44	57.22	1.53
IHL65	80.50	72.70	54.64	1.95
IHL175	79.00	70.07	65.66	2.04
Super303	78.08	70.20	65.10	1.96
Sakha104x IHL17	80.01	73.11	70.39	2.01
Sakha104x IHL65	82.00	73.55	69.71	2.33
Sakha104x IHL175	79.95	71.03	75.71	2.61
Sakha104xSuper303	80.10	72.27	70.06	2.15
Sakha106x IHL17	80.24	71.60	70.54	2.16
Sakha106x HL65	80.47	70.44	69.77	1.64
Sakha106x IHL175	79.56	71.68	72.59	2.08
Sakha106xSuper303	81.58	70.04	70.02	2.03
GZ11332x IHL17	76.65	71.66	72.05	1.75
GZ11332x IHL65	81.14	73.00	70.18	2.05
GZ11332x IHL175	80.35	70.35	69.87	2.09
GZ11332xSuper303	79.82	71.75	68.65	2.85
Sakha101x IHL17	79.40	71.10	68.46	2.31
Sakha101x IHL65	80.55	72.65	68.54	1.87
Sakha101x IHL175	79.42	71.07	68.52	2.16
Sakha101xSuper303	77.67	72.95	63.08	2.78
Sakha108x IHL17	80.46	72.00	64.19	2.41
Sakha108x IHL65	79.03	70.84	64.30	2.05
Sakha108x IHL175	79.66	72.26	62.28	2.18
Sakha108xSuper303	79.87	72.37	69.56	2.21
Sakha109x IHL17	80.59	71.62	70.03	2.48
Sakha109x IHL65	79.59	71.33	69.94	2.14
Sakha109x IHL175	81.57	73.12	68.12	2.67
Sakha109xSuper303	79.68	71.43	67.27	2.13
L.S.D 5%	1.05	0.66	0.38	0.14
L.S.D 1%	1.40	0.88	0.49	0.19

4.2. Combining ability analysis

Table 5 illustrates the analysis of combining ability for six morphophysiological traits, namely, days to 50% heading, plant height, No. of tillers plant-1, flag lea area, flag leaf angle and chlorophyll content. For all studied features, mean squares due to specific combining ability (SCA) were much higher than those of general combining ability (GCA), revealing that the non-additive gene action was responsible for the inheritance of these traits. These results are in line with those **of Ariful Islam et al., (2015), Mohamed et al., (2016), Kiani (2019), Singh et al., (2019), Abd-Aty et al., (2022), Bayoumi et al., (2022), El-Badaway et al., (2022), El-Gammaal et al., (2022), Kushal et al., (2023), Maring et al., (2023), Abo-Yousef et al., (2024), and Vennila (2024).** On the other hand, the predominance of additive genetic component in the inheritance of morphophysiological traits as reported by **Ayuba et al., (2022), Thakur (2023), Kumar et al., (2024), Modarrsi et al., (2024) Singh et al, (2025).**

4.2.1.A. General combining ability for morphophysiological traits:

Estimates of general combining ability (GCA) effects for the six morphophysiological traits are shown in **Table 11 and Figures 2-7.**

Results indicated that the lines Sakha104, GZ11332, Sakha108 and Sakha106, were highly significant negative GCA effects for days to 50% heading. These values were -6.71 **, -2.38 **, -1.46 **and -1.29 **respectively. In addition to the testers, IHL17 had highly significant negative GCA -2.65 ** andSuper303 was negative and significant -0.93 *. So, these parents could be considered the best general combiner for this trait.

Nine parents exhibited highly significant general combining ability effects for plant height, but three parents (GZ11332, Sakha101and Super303) had negative and highly significant GCA and their values were -1.10 **, -4.76 **and -2.41 ** respectively. While six parents were highly significant and positive values. They were undesirable general combining ability effects

Regarding No. of tillers / plant, the parents Sakha104 and Sakha109 revealed positive and highly significant general combining ability GCA effects. Their values recorded 0.65 ** and 2.32 **respectively. These parents seemed to be the best general combiners for this trait. In contrast, the parents Sakha106 and Sakha101 had negative and highly significant general combining ability effects

Respecting flag leaf area Sakha104, Sakha108, Sakha109 and Super303 recorded highly significant and positive general combining ability (GCA) effects (1.33 **, 1.73 **, 2.11 ** and 5.23 ** respectively). In addition to the five parents were negative and highly significant GCA effects (GZ11332, Sakha101, IHL17, IHL65 and IHL75).

The line Sakha104, Sakha106 and Sakha109 showed positive highly significant GCA effects. Sakha 109 was the highest general combining ability effects (4.30 **) followed by Sakha 104 (3.66 **). Only five parents GZ11332, Sakha101, Sakha108, IHL65and IHL175 exhibited negative and highly significant GCA effects are presented in table 11.

For Chlorophyll content the parents GZ11332, Sakha109, IHL17 and Super303 exhibited desirable significant and positive GCA effects. Line GZ11332 had the highest effects. Only two parents, Sakha101 and IHL75, had negative and highly significant general combining ability (GCA) effects. Their values were -1.95 ** and -1.15 ** respectively.

Table (11): Estimates of general combining ability effects for Morphophysiological traits in rice.

Genotypes	Days to 50% heading(days)	Plant height (cm)	No. of tillers / plant	Flag leaf area	Flag leaf Angle	Chloro-phyll con-tent
Lines						
Sakha104	-6.71 **	2.48 **	0.65 **	1.33 **	3.66 **	-0.13
Sakha106	-1.29 **	2.65 **	-1.68 **	-0.34	0.65 **	-0.96 *
GZ11332	-2.38 **	-1.10 **	0.07	-2.06 **	-3.31 **	1.40 **
Sakha101	10.04 **	-4.76 **	-1.10 **	-2.77 **	-4.31 **	-1.95 **
Sakha108	-1.46 **	0.95 **	-0.26	1.73 **	-0.99 **	0.44
Sakha109	1.79 **	-0.22	2.32 **	2.11 **	4.30 **	1.20 **
L.S.D gi5%	0.953	0.67	0.46	0.85	0.445	0.83
L.S.D gi 1%	1.266	0.89	0.61	1.13	0.592	1.10
L.S.D gi-gj 5%	1.35	0.94	0.65	1.20	0.63	1.17
L.S.D gi- gi 1%	1.79	1.25	0.86	1.59	0.84	1.55
Testers						
IHL17	-2.65 **	0.73 **	0.07	-0.96 **	0.36	0.93 **
IHL65	-0.54	0.82 **	-0.10	-2.87 **	-0.96 **	-0.74 *
IHL175	4.13 **	0.86 **	-0.21	-1.41 **	-0.51 **	-1.15 **
Super303	-0.93 *	-2.41 **	0.24	5.23 **	1.11 **	0.96 **
L.S.D gi5%	0.78	0.54	0.38	0.69	0.364	0.67
L.S.D gi1%	1.03	0.72	0.50	0.92	0.483	0.89
L.S.D gi-gj 5%	1.10	0.77	0.53	0.98	0.51	0.95
L.S.D gi-gj 1%	1.46	1.02	0.70	1.29	0.68	1.27

*** and ** significant at 0.05 and 0.01 levels of probability, respect ively.**

From the results in table (11), it could be concluded that Sakha 104 was good combiners for days to heading, Sakha 101 and Super 303 were good combiners for plant height. The Sakha 109 and Super 303 were good combiners for no. of tillers /plant, flag leaf area as well as, chlorophyll content

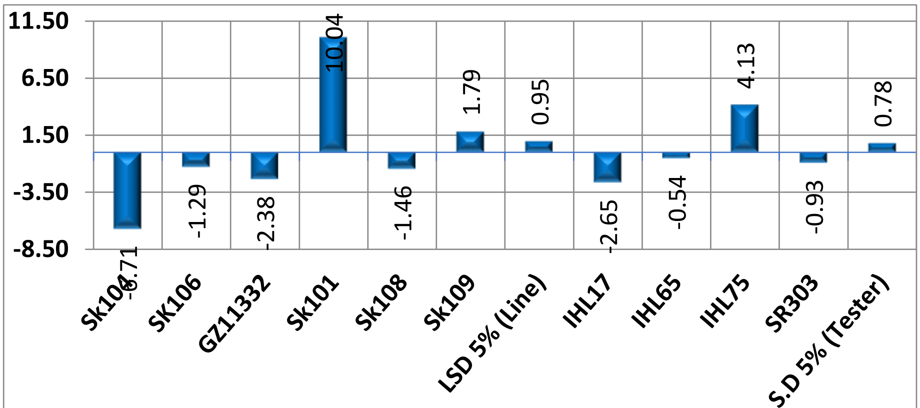


Fig. (2): GCA effects for days to 50% heading

SK= Sakha ، SR= Super

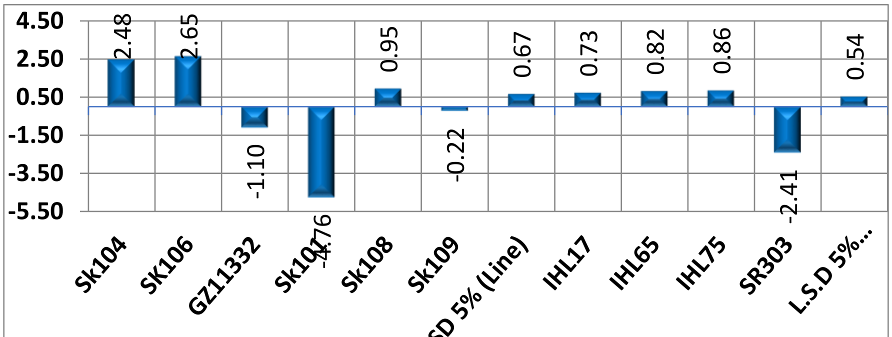


Fig. (3): GCA effects for plant height

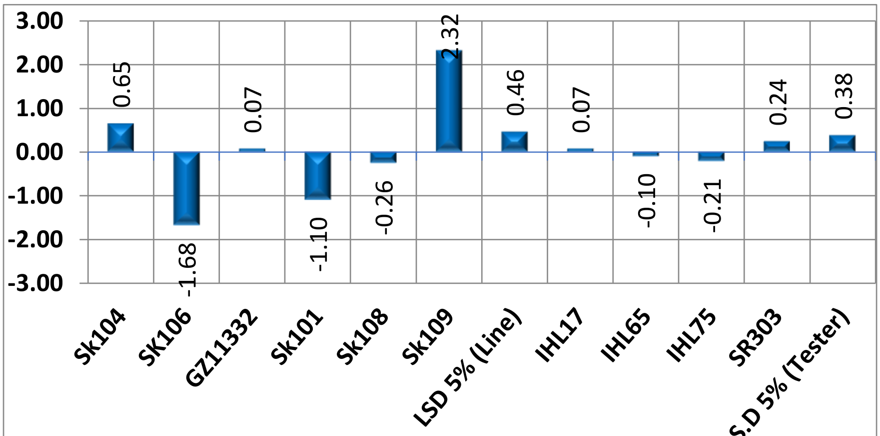


Fig. (4): GCA effects for number of tillrs/ plant

SK=Sakha ، SR= Super

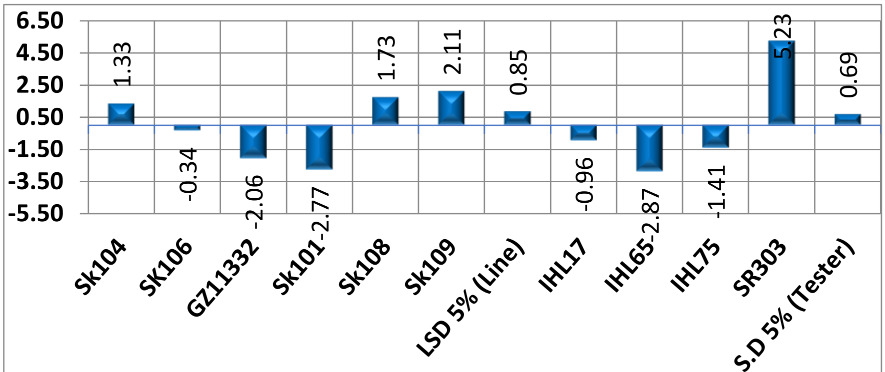


Fig. (5): GCA effects for flag leaf area

SK= Sakha ، SR= Super

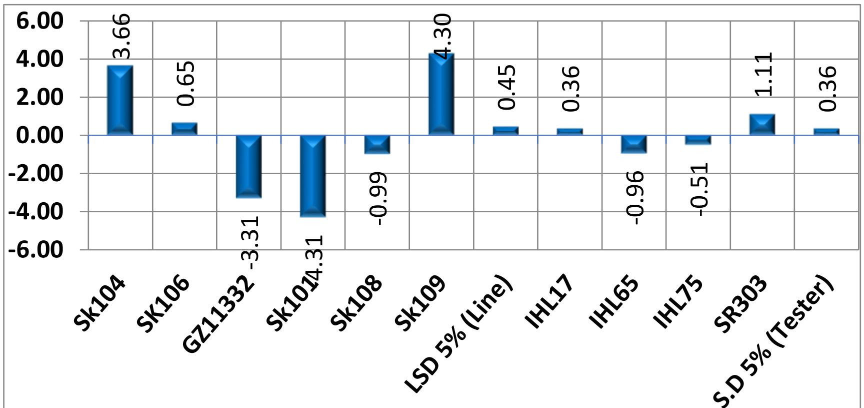


Fig. (6): GCA effects for flag leaf angle

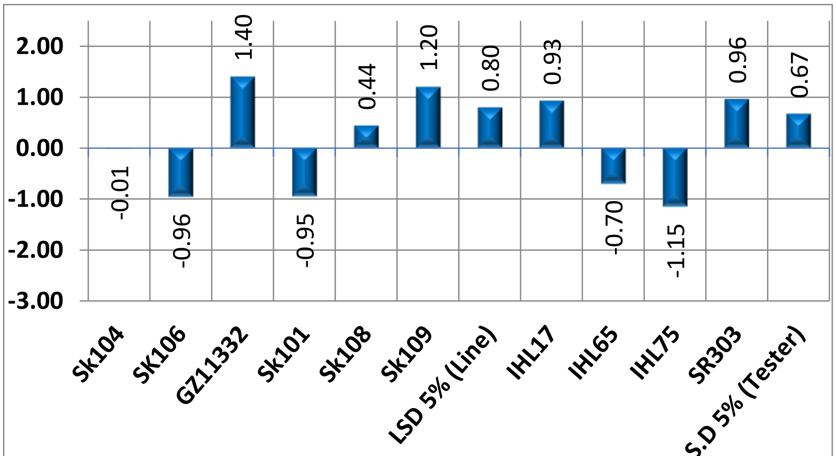


Fig. (7): GCA effects for chlorophyll content

4.2.1.B specific combining ability for morphophysiological traits:

Effects of specific combining ability (SCA) for the six morphophysiological traits (Days to 50% heading(days), Plant height (cm), No. of tillers / plant, Flag leaf area, Flag leaf angle and Chlorophyll content) are shown in Table12.

For days to 50% heading six crosses displayed significant and negative (desirable) for specific combining ability effects. These crosses seemed to be the best hybrid crosses. The highest values for specific combining ability effects were observed in Sakha109xSuper303, Sakha106xIHL175 and Sakha108xIHL65 with (-9.74 **, -7.71 ** and -7.54 **) respectively, While the lowest values showed in Sakha104xIHL75, GZ11332xIHL75 and Sakha101xIHL17 with (-5.29 **, -6.63 ** and -7.26 **). In addition, seven crosses had positive(undesirable) and highly significant and one cross was significant. The other crosses were non-significant effects.

Regarding plant height, four crosses, namely, Sakha104xSR303, Sakha106xIHL17, Sakha101xIHL175 and Sakha101xSuper303 expressed significant and negative SCA effects. However, the cross Sakha101xSuper303 recorded the most desirable effects for this trait (-2.69**).

For number of tillers plant-1, five crosses exhibited significantly positive SCA effects, however the most applicable effects were detected for the cross Sakha109xSuper303 which gave a value of 2.85** (Table 12).

Concerning flag area, the crosses GZ11332xSuper303, Sakha101xSuper303, Sakha108xIHL65 and Sakha108xIHL175 registered positive and highly significant. Where these crosses appeared to be the best crosses for specific combining ability effects. The highest values are revealed with Sakha108xIHL65 (3.78 **). Contrarily, the negative(undesirable) and highly significant showed with only two crosses (GZ11332xIHL175 and Sakha108xSuper303). Four crosses were negative and significant effects. The remaining crosses were non-significant SCA for flag leaf area.

Flag leaf angle nine crosses expressed desirable SCA effects. The eight crosses displayed highly significant positive for SCA effects. The highest cross was Sakha101xIHL65 with (4.87 **). Sakha106xSuper303 was positive and significant (1.15 *). Furthermore, seven crosses were negative and highly significant effects. So, these hybrids were undesirable for flag leaf angle. The other crosses were non-significant effects.

For chlorophyll content, among the 24 top crosses, SK109xSR303 had positive and highly significant with (2.39 **). This cross was the highest specific combining ability for Chlorophyll content. In addition, three crosses (Sakha104xIHL65, GZ11332xIHL75 and Sakha108xIHL75) exhibited positive and significant recorded values (2.09 *,1.82 * and 1.96 *) respectively. In contrast, Sakha109xIHL65 obtained negative value and highly significant (-3.21 **). Two crosses registered negative and significant effects. The other crosses had non-significant effects **(Table 12).**

From these results, could be concluded that, the cross Sakha 109xSuper 303 recorded the desirable specific combining ability effect for days to heading, number of tillers / plant and chlorophyll content, while the cross GZ11332 x Super 303 recorded the desirable SCA for flag leaf area and angle ,on the other sides, the cross Sakha 101 x Super 303 was recorded the desirable SCA for plant height indicating to the Super 303 was good combinor for most of morphological characters.

Table (12): Estimates of specific combining ability effects for some morpho-physiological traits in rice.

Genotypes	Days to 50% heading (days)	Plant height (cm)	No. of tillers / plant	Flag leaf area	Flag leaf angle	Chlorophyll content
Sakha104x IHL17	0.49	0.61	0.68	0.57	-3.93 **	0.24
Sakha104x IHL65	0.38	0.51	0.51	0.68	1.57 **	2.09 *
Sakha104x IHL175	-5.29 **	1.48 *	-1.04 *	-0.44	-2.21 **	-2.08 *
Sakha104xSR303	4.43 **	-2.59 **	-0.15	-0.81	4.57 **	-0.25
Sakha106x IHL17	3.07 **	-0.89	0.01	-1.27	-1.47 **	1.13
Sakha106x HL65	2.29 *	-1.99 **	0.18	1.35	-3.13 **	0.39
Sakha106x IHL175	-7.71 **	-0.69	2.29 **	-0.15	3.46 **	-0.94
Sakha106xSR303	2.35 *	3.57 **	-1.49 **	0.07	1.15 *	-0.58
GZ11332x IHL17	4.49 **	-0.81	-1.74 **	1.66	7.56 **	-0.38
GZ11332x IHL65	1.71	0.10	0.10	-2.23 *	0.21	-1.02
GZ11332x IHL175	-6.63 **	-0.61	1.21 **	-2.70 **	-0.58	1.82 *
GZ11332xSuper303	0.43	1.32	-0.57	3.26 **	-7.19 **	-0.42
Sakha101x IHL17	-7.26 **	2.11 **	1.10 *	-2.20 *	-0.78	-0.16
Sakha101x IHL65	-0.71	2.92 **	0.60	-2.20 *	4.87 **	0.78
Sakha101x IHL175	6.96 **	-2.34 **	-0.29	1.10	2.09 **	-0.66
Sakha101xSuper303	1.01	-2.69 **	-1.40 **	3.31 **	-6.19 **	0.05
Sakha108x IHL17	-1.10	-0.33	-0.74	-1.71 *	-0.77	-1.74 *
Sakha108x IHL65	-7.54 **	-0.95	0.76	3.78 **	-3.45 **	0.96
Sakha108x IHL175	7.13 **	1.01	-1.79 **	3.52 **	0.76	1.96 *
Sakha108xSuper303	1.51	0.27	1.76 **	-5.59 **	3.46 **	-1.18
Sakha109x IHL17	0.32	-0.69	0.68	2.95 **	-0.62	0.92
Sakha109x IHL65	3.88 **	-0.58	-2.15 **	-1.38	-0.07	-3.21 **
Sakha109x IHL175	5.54 **	1.16	-1.38 **	-1.34	-3.52 **	-0.10
Sakha109xSuper303	-9.74 **	0.11	2.85 **	-0.24	4.20 **	2.39 **
Sij 5%	1.91	1.33	0.92	1.69	0.89	1.65
Sij 1%	2.53	1.77	1.22	2.25	1.18	2.19
Sij-SKI 5%	2.69	1.88	1.30	2.40	1.26	2.33
Sij- SKI 1%	3.58	2.50	1.73	3.18	1.67	3.10

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

4.2.2. Combining ability for yield and its contributing traits:

The analysis of combining ability for seven yield and its components, viz, were shown in Table 7 mean square. For all studied features, specific combining ability mean squares were much higher than those of general combining ability, indicating that dominance and epistasis played an essential role in controlling such attributes. Similar results were obtained **by Babu and Sreelakshmi (2018), Singh et al., (2019), Abo-Yousef et al., (2020), Ayuba et al., (2022), El-Gammaal et al., (2022), Abd-Aty et al., (2023), Das et al., (2023), Kumar et al., (2024), Modarresi et al., (2024), Vennila (2024) and Sing et al.,(2025).** On the contrary, additive genetic action was responsible for yield and other traits according to the findings of **Aamer and Ibrahim (2020), Kushal et al., (2023), and Singh et al., (2025).**

4.2.2.A. General combining ability for yield and its contributing traits

The results for No. of panicles/ plant, Panicle length (cm), Panicle weight (g), Spikelet fertility, 1000 grain weight (g), Grain yield/ plant (g) and Harvest index % are presented in **Table 13 and Fig. 8-14.**

No. of panicles/ plant the estimates of general combining ability (GCA) effects were highly significant and positive (desirable) for two parents (Sakha109 and Super303). Sakha109 had the highest GCA effects for No. of panicles / plant (2.50 **). Indicated to Sakha 109 was good combiner for non. of panicle/plant. In addition, three parents (GZ11332, Sakha101and IHL65) were negative and highly significant (undesirable) effects with the values of -1.83 **, -1.08 ** and-0.64 ** respectively.

Regarding Panicle length Sakha104, Sakha108, Sakha109, IHL17and Super303 exhibited positive and highly significant general combining ability effects. These parents regarded as good combiners for panicle length. Sakha109 was the highest significant positive for panicle length (0.92 **). Only four parents were negative and highly significant.

Three parents (Sakha108, Sakha109 and Super303) recorded highly significant and positive GCA effects for panicle weight. Super 303 was the most significant positive (0.58 **), While GZ11332, Sakha101, IHL17and IHL65 revealed negative and highly significant (undesirable).

Respecting spikelet fertility, GCA effects were positive and highly significant for Sakha109 and Super303 with 0.85 ** and 0.54 ** respectively. These lines were the best combiners for spikelet fertility. The parents Sakha104 and IHL65 had negative and highly significant (undesirable). The other parents, GZ11332, Sakha101, Sakha108 and IHL17 exhibited non-significant GCA effects.

Three parents GZ11332, Sakha 109 and Super 303 showed positive and highly significant GCA effects for 1000grain weight. So, these parents adjusted as good general combining ability. Sakha109 were the highest general combining ability effects1.46 ** for 1000 grain weight. Contrarily Sakha104 and IHL75 investigated negative and highly significant general combining ability effects. Only Sakha106, Sakha 108 and IHL65 exhibited non- significant effects.

Among ten parents only five parents (GZ11332, Sakha108, Sakha109, IHL175 and Super303) were positive and highly significant GCA effects for grain yield /plant. These parents regarded as good combiners for grain yield/ plants. Super303 obtained the highest general combining effects (2.61 **). Furthermore, the other five parents registered negative and highly significant GCA effects.

Regarding harvest index trait, the best general combining ability effects (GCA) were recorded by Sakha106, Sakha109 and Super303 parents with values 1.62 **, 5.67 ** and 1.15 **. Contrarily, Sakha104, GZ11332, Sakha101and IHL65 had negative and highly significant GCA effects. Further, Sakha108 and IHL75 were non- significant effects.

Table (13): Estimates of general combining ability effects for yield and its components in rice.

Genotypes	No. of panicles/ plant	Panicle length (cm)	Panicle weight (g)	Spikelet fertility	1000 grain weight (g)	Grain yield/ plant (g)	Harvest index %
Lines							
Sakha104	**0.33**	**0.69 ****	**0.07**	**-0.70 ****	**-1.68 ****	**-3.24 ****	**-2.17 ****
Sakha106	**0.17**	**-1.14 ****	**0.02**	**-0.48 ***	**0.28**	**-2.23 ****	**1.62 ****
GZ11332	**-1.83 ****	**-0.51 ****	**-0.58 ****	**0.34**	**0.71 ****	**1.46 ****	**-0.89 ****
Sakha101	**-1.08 ****	**-0.48 ****	**-0.12 ****	**0.01**	**-0.85 ****	**-2.96 ****	**-4.35 ****
Sakha108	**-0.08**	**0.51 ****	**0.21 ****	**-0.01**	**0.08**	**2.78 ****	**0.12**
Sakha109	**2.50 ****	**0.92 ****	**0.40 ****	**0.85 ****	**1.46 ****	**4.20 ****	**5.67 ****
L.S.D gi 5%	**0.39**	**0.15**	**0.08**	**0.37**	**0.44**	**0.56**	**0.59**
L.S.D gi 1%	**0.514**	**0.19**	**0.11**	**0.50**	**0.59**	**0.75**	**0.78**
L.S.D gi-gj 5%	**0.55**	**0.21**	**0.11**	**0.53**	**0.63**	**0.79**	**0.83**
L.S.D gi- gj 1%	**0.73**	**0.27**	**0.15**	**0.70**	**0.83**	**1.05**	**1.10**
Testers							
IHL17	**0.14**	**0.53 ****	**-0.15 ****	**-0.18**	**-0.48 ***	**-1.61 ****	**0.14**
IHL65	**-0.64 ****	**-0.96 ****	**-0.36 ****	**-0.71 ****	**0.06**	**-2.41 ****	**-1.27 ****
IHL175	**-0.31**	**-0.04**	**-0.07 ***	**0.34 ***	**-0.14**	**1.42 ****	**-0.01**
Super303	**0.81 ****	**0.46 ****	**0.58 ****	**0.54 ****	**0.56 ****	**2.61 ****	**1.15 ****
L.S.D gi 5%	**0.32**	**0.12**	**0.07**	**0.31**	**0.36**	**0.46**	**0.48**
L.S.D gi1%	**0.42**	**0.16**	**0.09**	**0.41**	**0.48**	**0.61**	**0.64**
L.S.D gi-gj 5%	**0.45**	**0.17**	**0.09**	**0.43**	**0.51**	**0.65**	**0.68**
L.S.D gi-gj 1%	**0.59**	**0.22**	**0.12**	**0. 57**	**0.68**	**0.86**	**0.89**

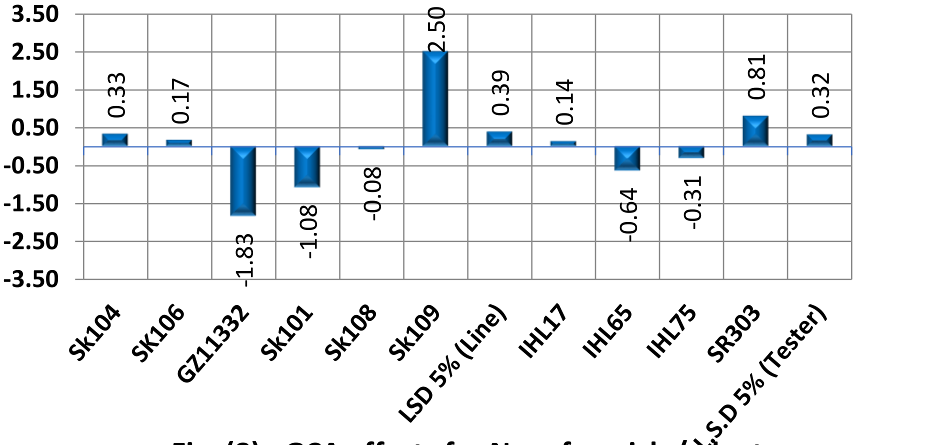


Fig. (8): GCA effects for No. of panicle/ plant

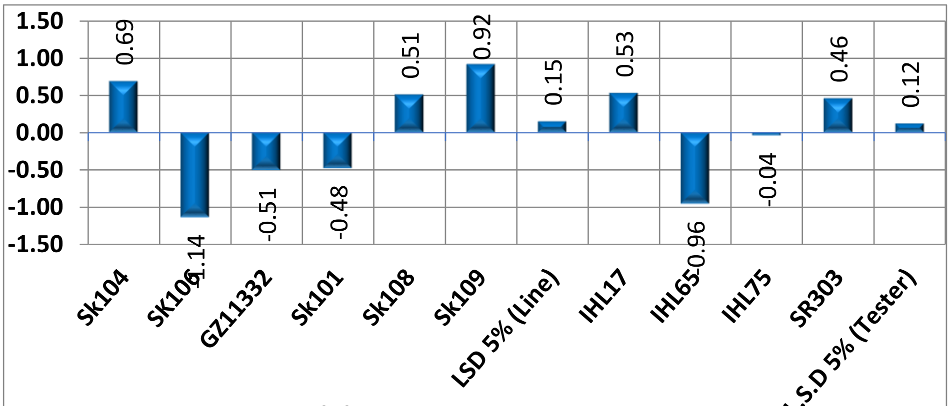


Fig. (9): GCA effects for panicle length

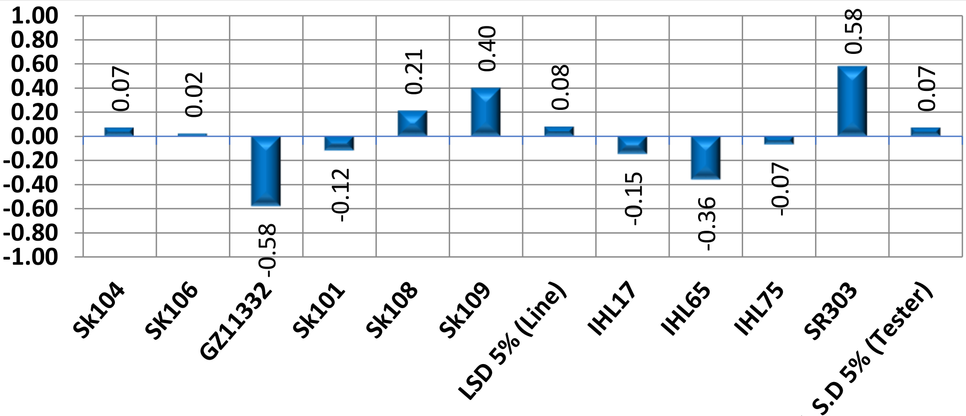


Fig. (10): GCA effects for panicle weight

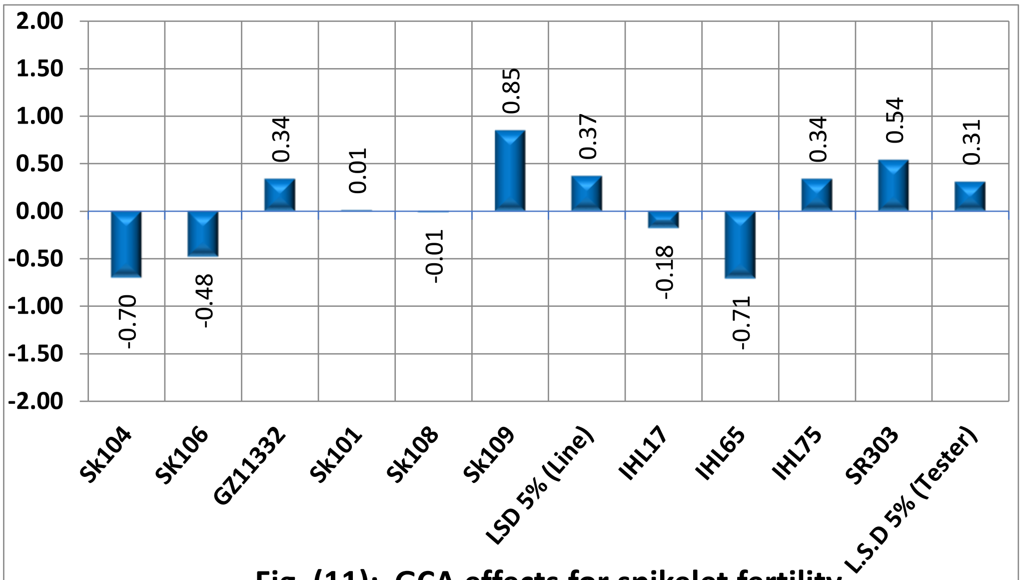


Fig. (11): GCA effects for spikelet fertility

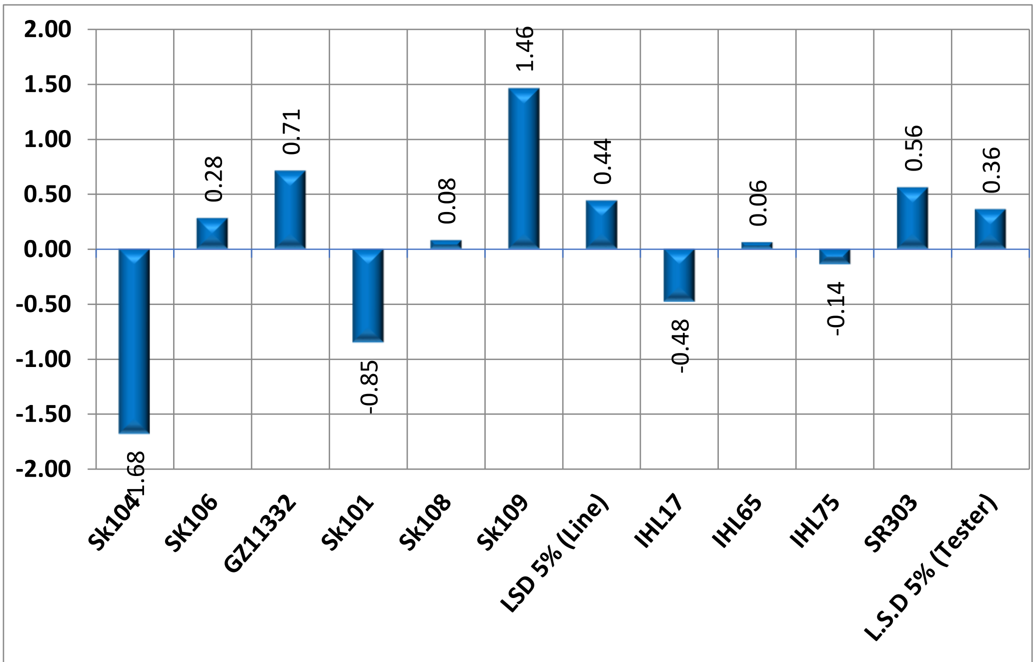


Fig. (12): GCA effects for 1000 grain weight

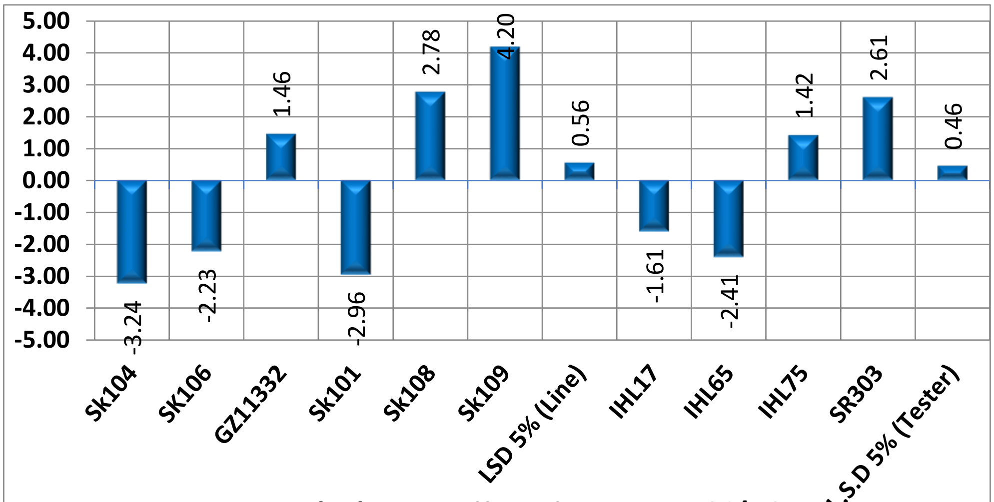


Fig. (13): GCA effects for grain yield/ plant

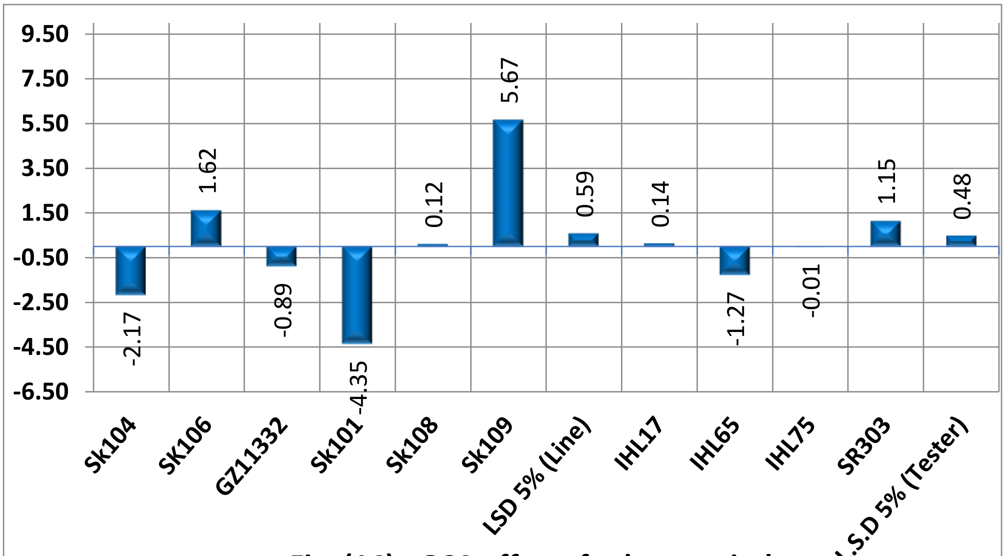


Fig. (14): GCA effects for harvest index

4.2.2.B. Specific combining ability for yield and its components:

Estimates of SCA effects for yield and its related traits (No. of panicles/ plant, Panicle length (cm), Panicle weight (g), Spikelet fertility, 1000 grain weight (g), Grain yield/ plant (g) and Harvest index % are listed are presented in Table 14.

Regarding the number of panicles plant-1, four out of 24 crosses showed positive and highly significant SCA effects which were Sakha106xIHL75, Sk101xIHL17, Sakha108xSuper303 and Sakha109xSuper303. These crosses could be considered as good combiners for No. of panicles/ plant. The highest crosses were Sakha109xSuper303 with 2.78 ** value. The cross Sakha101xIHL65 was positive and significant .14 crosses displayed non-significant SCA effects.

Panicle length was positive(desirable) and significant for nine crosses out of 24 crosses. These crosses represented the best specific combing ability effects. The highest cross was Sakha106xIHL175 with 1.51 **. Furthermore, seven crosses exhibited negative and highly significant effects. Seven crosses recorded non-significant effects. Sakha104xIHL175 cross had negative and significant.

Panicle weight, four crosses demonstrated positive and significant SCA effects. These crosses are regarded as good combiners for panicle weight. The cross GZ11332xIHL67 explained the highest specific combining ability effects with 0.69 **. Moreover, five crosses asserted negative(undesirable) and highly significant effects.

Spikelet fertility was positive and highly significant with four crosses which could be considered as good specific combining ability effects. The highest crosses effects represented in Sakha101xIHL65 with 1.38 **. Sk106xIHL65 cross had positive and significant effects. Concerning, four crosses observed highly significant negative (undesirable) effects.

Concerning 1000 grain weight, the Sakha108xSuper303 and Sakha106xPIHL175 crosses exhibited positive and highly significant effects with 1.58 ** and1.45 **. These crosses seemed to be the best specific combining ability. Sakha 109xIHL17 had positive and significant values with 0.97 *. Moreover, Sakha106xSuper303 and Sakha101xIHL175 investigated negative and highly significant effects. Only the cross Sakha108xIHL175 had negative and significant effects.

For grain yield plant-1, nine crosses expressed significantly positive SCA effects. However, the cross Sakha106xIHL175 produced the highest effects (3.86**) followed by the cross Sakha109xIHL17 (3.55**) then the cross Sakha101x IHL65 (2.87**) (Table 14).

Respecting harvest index, the results revealed that the most desirable effects for this trait were detected for 8 crosses. These crosses registered positive and highly significant effects which are regarded as good specific combining ability. The cross Sakha109xIHL17 was positive and significant, While the undesirable crosses (negative) with highly significant were detected by six crosses.

Table (14): Estimates of specific combining ability effects for yield and its related

Genotypes	No. of panicles/ plant	Panicle length (cm)	Panicle weight (g)	Spikelet fertility	1000 grain weight (g)	Grain yield/ plant (g)	Harvest index %
Sakha104x	0.28	-0.59 **	-0.03	-0.16	0.38	0.14	-3.01 **
Sakha104x	0.72	1.40 **	0.06	-1.41 **	0.28	1.25 *	2.91 **
Sakha104x	-0.28	-0.31 *	-0.06	1.08 **	-0.18	0.65	2.07 **
Sakha104xSR30	-0.72	-0.50 **	0.03	0.49	-0.49	-2.04 **	-1.96 **
Sakha106x	-0.89 *	0.23	-0.23 **	-0.36	-0.38	-2.52 **	-0.29
Sakha106x HL65	0.56	-0.25	0.15	0.94 *	0.12	-0.61	0.92
Sakha106x	1.89	1.51 **	0.01	1.00 **	1.45 **	3.86 **	2.03 **
Sakha106xSu-	-1.56	-1.49 **	0.07	-1.58 **	-1.19 **	-0.73	-2.66 **
GZ11332x	-0.22	0.32 *	-0.38 **	0.28	-0.22	1.29 *	2.23 **
GZ11332x	0.22	0.95 **	0.69 **	-0.15	0.53	1.52 **	1.74 **
GZ11332x IHL17	0.22	-1.06 **	-0.35 **	0.13	-0.16	-1.10	-0.12
GZ11332xSR303	-0.22	-0.21	0.04	-0.26	-0.15	-1.70 **	-3.85 **
Sakha101x	1.03	0.50 **	0.20 *	-0.02	-0.18	-3.44 **	0.87
Sakha101x	0.81 *	-0.84 **	-0.45 **	1.38 **	0.45	2.87 **	2.47 **
Sakha101x	0.14	-0.01	0.11	-1.53 **	-0.39	-0.70	-2.31 **
Sakha101xSu-	-1.97	0.34 *	0.14	0.17	0.11	1.26 *	-1.03
Sakha108x	-0.64	-0.68 **	-0.09	-0.75 *	-0.58	0.97	-1.20 *
Sakha108x	0.47	0.38 *	0.01	0.63	0.02	1.32 *	-1.53 *
Sakha108x	-1.53	-0.29	0.25	-0.60	-1.02 *	-2.73 **	-2.69 **
SK108xSR303	1.69	0.59 **	-0.18 *	0.73	1.58 **	0.44	5.42 **
Sakha109x	0.44	0.21	0.53	1.01 **	0.97 *	3.55 **	1.40 *
Sakha109x	-2.78	-1.64 **	-0.46	-1.38 **	-1.40 **	-6.36 **	-6.51 **
Sakha109x	-0.44	0.16	0.03	-0.08	0.30	0.02	1.03
Sakha109xSu-	2.78	1.26 **	-0.10	0.45	0.13	2.78 **	4.08 **
Sij 5%	0.77	0.29	0.16	0.75	0.89	1.12	1.17
Sij 1%	1.03	0.39	0.21	0.99	1.18	1.49	1.56
Sij-SKI 5%	1.09	0.41	0.23	1.06	1.26	1.59	1.66
Sij -SKI 1%	1.45	0.55	0.30	1.40	1.67	2.10	2.20

The cross Sakha 101×IHL65 for Spikelet fertility and grain yield, the cross Sakha 108 × Super 303 for 1000 grain weight and harvest index that, Mean the two tester IHL65 and Super 303 were the good combiners to improvement the yield components.

4.2.3. Combining ability for Grain Quality traits:

The combining ability analysis of four quality traits, namely, hulling%, milling%, head rice recovery and grain shape was presented in Table 9. The obtained results revealed that dominance and epistasis are responsible for all quality traits since SCA mean squares were much higher than those of GCA ones. These findings are in line with those previously reported by **Buelah et al., (2020), Kumar et al., (2021), El-Gammaal et al., (2022), Shivastav et al., (2022), Kushal et al., (2023), Kumar and Pandy (2023), El-Naem et al., (2024), Lingaiah et al., (2024), Santhiya et al., (2024), and Thang (2024).** They found that the non-additive component was predominant for most quality traits. Also, one parental line and two testers proved to be good combiners for quality traits.

4.2.3.A. General combining ability for grain quality traits:

The effects of GCA for the four grain quality traits (Hulling %, Milling %, Head rice recovery and Grain shape are shown in Table 15 and Fig. 15-18.

For Hulling the GCA effects were positive and highly significant for Sakha104 and IHL65 with 0.53 ** and 0.81 ** respectively. These parents were the best general combiners for hilling. In addition, Sakha101 and IHL17 had negative and highly significant (-0.73 ** and -0.55 ** respectively). The other parents (Sakhak108 and Super303) exhibited non- significant effects.

Regarding milling trait, the highest general combining ability effect was recorded by the line Sakha104 (0.65 **) followed by IHL65 (0.44 **). These parents seemed to be good combiners for milling. Conversely, Sakha106 and IHL175 were negative(undesirable) and had highly significant GCA effects. Only three parents, Sakha101, Sakha108 and IHL17 revealed non- significant effects.

Respecting head rice recovery, seven parents out of ten parents were positive and highly significant general combining ability effects. The best parents were Sakha104, Sakha106, GZ11332, Sakha109, IHL17, IHL65 and IHL175. The highest GCA effects recorded by Sk104 (2.44 **). The other three parents, Sakha101, Sakha108 and Super303, had negative and highly significant effects.

For grain shape, Sakha109 (0.16 **) and Super303 (0.23 **) parents investigated highly significant positive. The results revealed that in Sakha106, IHL17 and IHL65 parents with -0.24 **, -0.07 ** and -0.13 ** respectively were negative and highly significant. The other parents, GZ11332, Sakha108 andIHL75, were non-significant effects.

Table (15): Estimates of general combining ability effects for some qual-

Genotypes	Hulling %	Milling %	Head rice recovery	Grain shape
Lines				
Sakha104	0.53 **	0.65 **	2.44 **	0.06 *
Sakha106	0.47 *	-0.90 **	1.70 **	-0.24 **
GZ11332	-0.50 *	-0.15	1.16 **	-0.03
Sakha101	-0.73 **	0.10	-1.88 **	0.07 *
Sakha108	-0.20	0.03	-3.80 **	-0.02
Sakha109	0.42 *	0.27 *	0.38 **	0.16 **
L.S.D gi 5%	0.37	0.23	0.13	0.05
L.S.D gi 1%	0.50	0.31	0.18	0.07
L.S.D gi-gj	0.53	0.33	0.19	0.07
L.S.D gi-gj	0.70	0.44	0.25	0.10
Testers				
IHL17	-0.55 **	0.13	0.17 **	-0.07 **
IHL65	0.81 **	0.44 **	0.70 **	-0.13 **
IHL175	-0.34 *	-0.79 **	1.13 **	-0.03
Super303	0.08	0.22 *	-2.00 **	0.23 **
L.S.D gi 5%	0.31	0.19	0.11	0.04
L.S.D gi1%	0.41	0.25	0.14	0.06
L.S.D gi-gj	0.43	0.27	0.15	0.06
L.S.D gi-gj	0.57	0.36	0.20	0.08

From the results in **table (15**) could be concluded that , the Sakha 104 recorded the desirable GCA for hulling, milling and head rice recovery, the Sakha 109 recorded the desirable GCA for grain shape , while the tester IHL65 recorded the desirable GCA for hulling and milling ,Also the tester IHL175 recorded the desirable GCA for head rice recoveary and Super 303 was recorded the desirable GCA for grain shape.

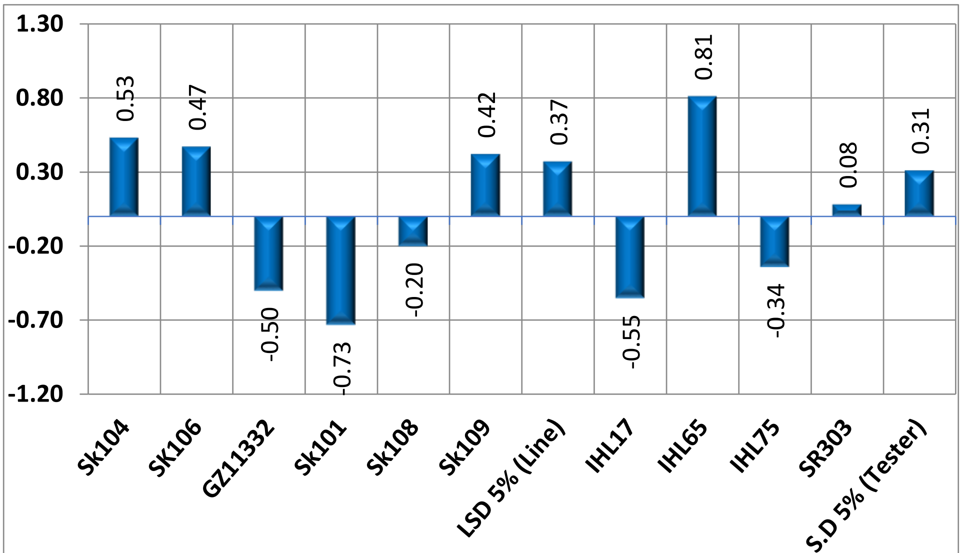


Fig. (15): GCA effects for hulling

SK = Sakha ‘SR= Super

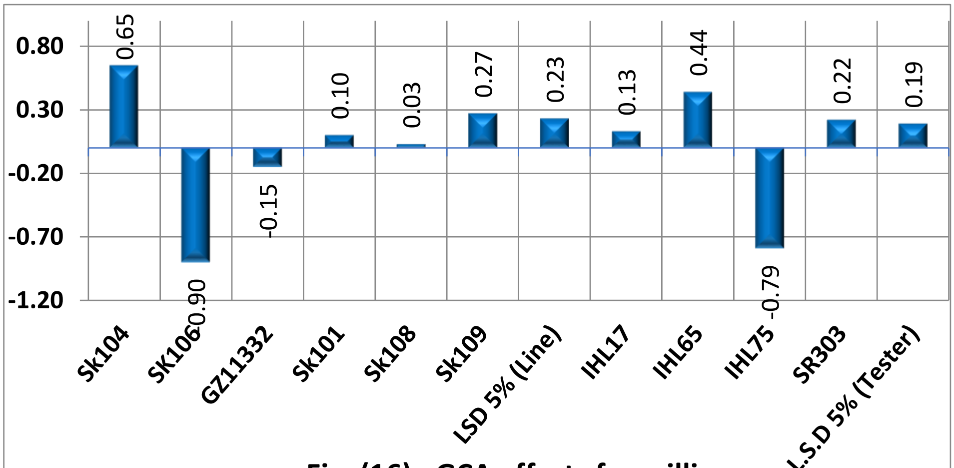


Fig. (16): GCA effects for milling

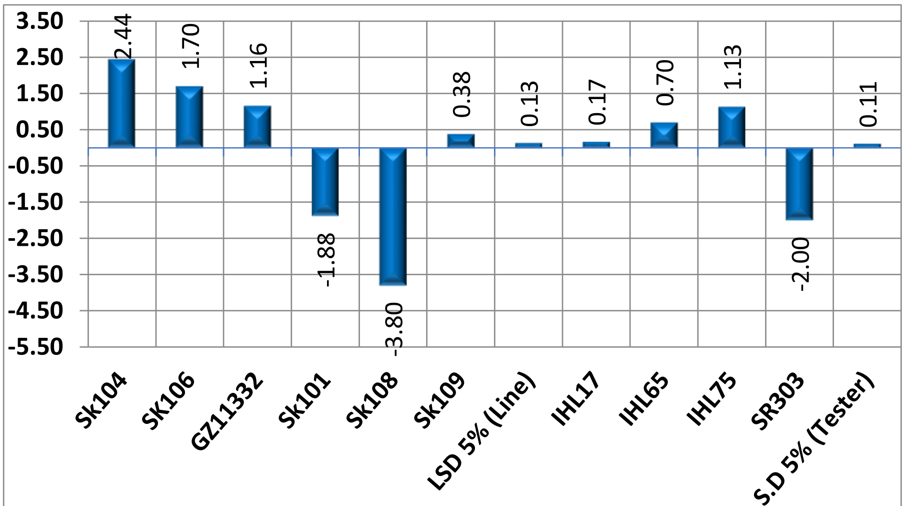


Fig. (17): GCA effects for head rice

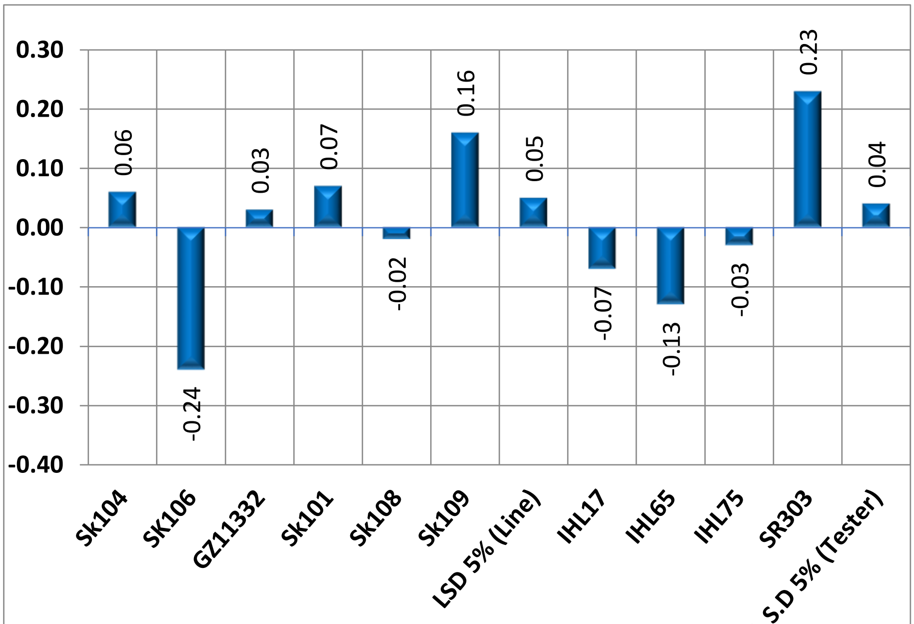


Fig. (18): GCA effects for grain shape

4.2.3.B. Specific combining ability for grain quality traits:

Estimates of specific combining ability effects for all quality characteristics are shown in Table 16.

Respecting hulling trait, Data insinuated that five out of 24 crosses were positive and significant specific combining ability (SCA) effects. The highest crosses were Sakha108xIHL17, GZ11332xIHL75 andSK109xSuper303 with1.22 **, 1.19 ** and1.08 **, respectively. These crosses could be considered as good SCA effects. In contrast, GZ11332xIHL17 and Sakha101xSuper303 exhibited negative and highly significant values.

The most desirable effects for milling trait were revealed for five crosses which were positive and highly significant values. All crosses that obtained highly significant positive seemed to be the best specific combining ability. The highest effect was showed with Sakha106xIHL75 cross with1.53 **. Two crosses (Sakha106xIHL17 and Sakha104xIHL17) were positive and significant SCA effects.

Regarding head rice recovery, the results in table 16 explained that ten crosses gave the best specific combining ability effects which were positive and highly significant. The highest cross was Sakha108xIHL65 with 4.23 **. Concerning, 11 crosses had highly significant negative SCA effects. These crosses were undesirable for head rice recovery.

Concerning grain shape, nine crosses had positive and highly significant values. The highest cross was GZ11332xSuper303 with 0.44 **, while the lowest cross was Sakha104xIHL65 with 0.19 **. Conversely, the highest negative and highly significant cross was GZ11332xIHL17 with -0.36 **.

Table (16): Estimates of specific combining ability effects for some quality traits in rice.

Genotypes	Hulling %	Milling %	Head rice recovery	Grain shape
Sakha104x IHL17	0.04	0.49 *	-1.24 **	-0.20 **
Sakha104x IHL65	0.68	0.63 **	-2.46 **	0.19 **
Sakha104x IHL175	-0.23	-0.67 **	3.12 **	0.36 **
Sakha104xSuper303	-0.50	-0.44	0.59 **	-0.35 **
Sakha106x IHL17	0.32	0.53 *	-0.36 **	0.25 **
Sakha106x HL65	-0.80 *	-0.93 **	-1.66 **	-0.20 **
Sakha106x IHL175	-0.56	1.53 **	0.73 **	0.13 *
Sakha106xSuper303	1.04 **	-1.12 **	1.28 **	-0.18 **
GZ11332x IHL17	-2.29 **	-0.16	1.69 **	-0.36 **
GZ11332x IHL65	0.85 *	0.87 **	-0.71 **	-0.01
GZ11332x IHL175	1.19 **	-0.55 *	-1.44 **	-0.07
GZ11332xSuper303	0.25	-0.17	0.46 **	0.44 **
Sakha101x IHL17	0.69	-0.97 **	1.14 **	0.11 *
Sakha101x IHL65	0.48	0.27	0.69 **	-0.28 **
Sakha101x IHL175	0.50	-0.08	0.25	-0.10
Sakha101xSuper303	-1.67 **	0.78 **	-2.07 **	0.27 **
Sakha108x IHL17	1.22 **	-0.01	-1.21 **	0.29 **
Sakha108x IHL65	-0.59	0.09	4.23 **	0.07
Sakha108x IHL175	-0.42	-0.25	-2.06 **	-0.12 *
Sakha108xSuper303	-0.21	0.17	-0.96 **	-0.24 **
Sakha109x IHL17	0.01	0.13	-0.02	-0.09
Sakha109x IHL65	-0.62	-0.93 **	-0.08	0.24 **
Sakha109x IHL175	-0.48	0.01	-0.60 **	-0.21 **
Sakha109xSuper303	1.08 **	0.78 **	0.70 **	0.06
Sij 5%	0.75	0.47	0.27	0.10
Sij 1%	1.00	0.62	0.35	0.14
Sij-SKI 5%	1.06	0.66	0.38	0.14
Sij -SKI 1%	1.40	0.88	0.49	0.19

From the results **in table (16)** it could be concluded that, the cross Sakha 108 × IHL17, Sakha 106 × IHL17, Sakha 108 ×IHL65 and GZ11332 ×Super 303 were recorded the desirable SCA for hulling, milling, head rice recoveary and grain shape respectively.

4.3 Heterosis

In tables (5,7,9) the results revealed that, mean square of crosses and parents vs. crosses was highly significant. These explained the presence of heterosis in F1 generation. Heterosis is estimated relative to both mid parent and better parent for morphophysiological, yield and its components trait and some quality traits.

4.3.1. Heterosis for morphophysiological traits

Heterosis values relative to mid-parent (MP) and better-parent (BP) for the six morphophysiological traits were shown in **Table 17.**

For days to 50% heading, sixteen and nineteen crosses expressed significantly negative effects relative to MP and BP heterosis, respectively. However, the best heterotic values regarding this trait were detected for the cross Sakha104xIHL17 (-24.96 %), and the cross Sakha108xIHL65 (-26.81%) for the respective cases.

Regarding plant height, none of the studied crosses exhibited significant desirable heterosis relative to mid-parent. However, two crosses, namely Sakha104xSuper303 (-3.14%) and Sakha101xSuper 303 (-2.72%) had significantly negative heterosis relative to better parent **(Table 17).**

Twenty-two and seventeen crosses, respectively, showed favorable heterotic effects in relation to mid parent and better parent in terms of the number of tiller plants per plant. Furthermore, for the respective heterosis types, the cross GZ11332xIHL175 had the best heterotic effects, which were 44.26 and 44.22%.

For flag area, twenty-one crosses insinuated significantly positive MP and BP heterosis, whereas the cross Sakha109xSuper303 exhibited the best values recording 41.06 and 36.45% for both types of heterosis, respectively **(Table 17).**

Desirable heterosis values in relation to mid parent and better parent were found for 23 and 18 crosses, respectively, in terms of flag leaf angle. The highest results, however, were obtained by cross Sakha109xIHL17, which recorded 82.93 and 72.47% of the corresponding cases.

For chlorophyll content, the most desirable mid parent (MP) and better parent (BP) heterosis were detected for the cross Sakha108xIHL65 giving 31.11% for MP and 22.38% for BP heterosis. Similar results were reported by Abd El-Aty et al., (2022), Ayuba et al., (2022), Sunny et al., (2022), Kushal et al., (2023), El-Naem et al., (2024), and Singh et al., (2025).

4.3.2. Heterosis for yield and its contributing traits

Data in Table 18 manifested both types of heterosis for the seven traits of yield and its contributing traits. For number of panicles plant-1, twenty-three (MP) and twenty-one (BP) crosses expressed significantly positive heterotic values for this trait. However, the most desirable heterosis was obtained for the cross Sakha109xIHL175 being 12.86 and 35.59% for MP and BP, respectively.

Regarding panicle length, twenty-one and nineteen crosses expressed desirable mid-parent and better-parent heterosis, respectively. Moreover, the cross Sakha109xSuper303 gave the most useful heterosis being 23.39% (MP) and 23.06% (BP) as shown in Table 18.

In terms of panicle weight, twenty-two and nineteen crosses, respectively, showed considerably positive heterosis in comparison to the mid -parent and better-parent. For the respective forms of heterosis, the cross Sakha108xIHL175 showed the best values, which were 40.95 and 29.80%.

Twenty-three and eighteen crosses showed desirable mid-parent and better-parent heterosis, respectively, for spikelet fertility. In the meantime, the best heterotic values for each heterotic type were 11.60 and 9.78% in the cross Sakha104xIHL175 respectively.

For 1000 grain weight, all the studied crosses expressed desirable heterotic values relative to mid-parent, while eighteen crosses gave desirable better heterosis for this trait. The best heterotic values were 17.45 and 14.17% for mid-parent and better-parent heterosis, respectively, according to the cross Sakha106xIHL175 results.

Twenty-one and eighteen top crosses, respectively, produced considerably positive heterotic values in relation to mid-parent and better-parent in terms of grain yield plant-1. The cross Sakha109xSuper303 (37.93%) in relation to MP and the cross Sakha109xIHL17 (35.57%) in relation to BP heterosis, however, showed the best heterotic values.

Twenty-three and fifteen crosses, respectively, displayed desirable MP and BP heterosis in relation to the harvest index. However, as seen in Table 18, the cross Sakha109xSuper303 produced the most appropriate heterosis, recording 64.84% (MP) and 54.03% (BP). The results are in line with those obtained by **Bayoumi et al., (2022), El-Badawy et al., (2022), El-Gammaal et al., (2022), Neupane (2022), Kushal et al., (2023), El-Naem et al., (2024), and Singh et al., (2025).**

4.3.3. Heterosis for grain quality traits

Table 19 displays the heterosis values in relation to mid-parent and better parent. The findings made it clear that, in comparison to MP and BP, seventeen and five crosses, respectively, exhibited suitable heterosis values for hulling%. The most desired heterotic values, 5.11 and 4.48% for the corresponding forms of heterosis, were displayed by the cross Sakha106xSuper303.

In comparison to mid-parent and better-parent, respectively, 19 and 15 crosses showed considerably favorable heterosis for milling percentage. However, the crosses Sakha108xSuper303 (4.39%) and

Sakha109xSuper303 (4.154%) showed the most suitable heterosis values.

Twenty-two and twenty-one crosses, respectively, showed satisfactory heterotic values in relation to MP and BP heterosis in terms of head rice recovery. In the interim, the cross Sakha109xIHL65 produced the best results, recording 29.71 and 28.18%, respectively.

For grain shape the positive and significant heterosis over mid parent ranged from 2.13* for cross Sakha106xIHL75 to 49.13** for cross GZ11332xSuper303. The negative and highly significant heterosis showed with Sakha106xIHL65, Sakha101xIHL65 and Sakha108xIHL75. Relative to better parent, the heterosis was highly significant positive in all crosses except three crosses which ranged from 1.59** for cross Sakha108xIHL65 to 45.58** for cross GZ11332xSuper303. while the three crosses were negative and highly significant represented in Sakha108xIHL75, GZ11332xIHL17 and Sk106xIHL65 (Table 19). **Similar results were reported by Renuka et al., (2019), El-Gammaal et al., (2022), Kushal et al., (2023), and Santhiya et al., (2024).**

Conclusion

From the previous results of mean performance and combining ability as well as heterosis values, it is clear that the cross Sakha109xSuper303 exhibited the most desirable values for grain yield plant and most of its attribute traits. As a result, this cross is promising and may be applied in upcoming rice breeding initiatives to improve yield potentiality and quality.

Table (17): Heterosis values relative to mid parent and better parent for some morphophysiological traits in rice.

Genotypes	Days to%50 heading(days)		Plant height (cm)		No. of tillers / plant		Flag leaf area		Flag leaf angle		Chlorophyll conten	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
Sakha104x IHL17	-24.96**	-25.98**	7.92**	2.83**	8.18**	3.61**	20.28**	18.06**	27.92**	1.37*	11.78**	11.30**
Sakha104x IHL65	-23.24**	-24.40**	12.18**	2.83**	12.58**	2.41**	12.53**	12.01**	31.85**	13.19**	18.08**	12.73**
Sakha104x IHL175	-21.27**	-22.98**	10.92**	3.77**	11.11**	-3.61**	14.01**	14.01**	9.45**	3.77**	2.02	1.10
Sakha104xSR303	-11.34**	-18.63**	0.65	-3.14**	3.07**	1.20	32.03**	31.42**	37.93**	27.52**	9.78**	8.47**
Sakha106x IHL17	-9.88**	-18.73**	8.21**	4.53**	6.94**	1.32*	16.42**	12.50**	22.31**	-4.68**	11.52**	11.45**
Sakha106x HL65	-8.70**	-17.77**	11.50**	3.56**	13.24**	13.24**	15.63**	9.26**	3.60**	-12.73**	10.90**	5.50**
Sakha106x IHL175	-10.45**	-16.56**	10.58**	4.85**	28.68**	22.06**	16.10**	10.19**	14.56**	6.31**	2.43*	1.14
Sakha106xSuper303	1.68	1.12	8.46**	5.83**	-3.41**	-9.50**	36.85**	30.46**	15.32**	4.41**	6.47**	5.59**
GZ11332x IHL17	-9.85**	-18.43**	5.76**	3.31**	12.41**	1.32*	15.99**	15.99**	71.63**	53.16**	12.18**	10.80**
GZ11332x IHL65	-10.67**	-19.28**	11.11**	4.30**	27.13**	20.59**	-3.07**	-5.30**	22.58**	20.25**	11.87**	5.12**
GZ11332x IHL175	-10.76**	-16.56**	8.12**	3.64**	40.26**	39.22**	0.20	-1.66	8.05**	-1.05	13.97**	11.10**
GZ11332xSuper303	-2.05	-2.23	3.69**	2.32*	14.89**	1.25	36.49**	34.58**	-6.51**	-12.22**	11.30**	10.78**
Sakha101x IHL17	-9.18**	-17.82**	8.13**	7.57**	10.07**	7.89**	6.90**	2.79*	58.97**	50.00**	1.43	-2.53*
Sakha101x IHL65	-0.67	-10.24**	13.64**	9.65**	13.48**	9.59**	-1.31	-7.19**	61.83**	39.47**	4.59**	-4.23**
Sakha101x IHL175	16.32**	8.77**	5.63**	4.15**	14.93**	5.48**	13.19**	6.90**	32.00**	4.21**	-3.58**	-8.52**
Sakha101xSuper303	12.48**	12.27**	-1.21	-2.72**	-1.96**	-6.25**	39.90**	32.71**	8.97**	-12.22**	1.27	-1.94
Sakha108x IHL17	-20.25**	-22.66**	8.71**	6.53**	2.60**	1.28	23.72**	17.17**	33.77**	11.96**	20.94**	7.73**
Sakha108x IHL65	-24.42**	-26.81**	12.57**	6.00**	13.70**	6.41**	31.30**	21.66**	8.33**	-1.09	31.11**	22.38**
Sakha108x IHL175	-2.75*	-3.22*	12.31**	8.00**	7.91**	-3.85**	35.53**	26.12**	12.28**	10.51**	27.45**	14.88**
Sakha108xSuper303	-7.24**	-13.50**	5.05**	4.00**	10.13**	8.75**	28.80**	20.37**	29.58**	28.17**	21.57**	7.56**
Sakha109x IHL17	-11.33**	-18.43**	5.88**	2.61**	26.39**	19.74**	34.31**	31.73**	82.93**	72.42**	20.73**	16.39**
Sakha109x IHL65	-5.90**	-13.55**	10.35**	2.80**	20.59**	20.59**	13.15**	8.48**	78.63**	53.95**	11.24**	9.66**
Sakha109x IHL175	4.44**	-0.65	9.90**	4.53**	30.23**	23.53**	18.05**	13.68**	44.00**	13.68**	14.19**	11.51**
Sakha109xSuper303	-10.42**	-11.87**	2.50**	0.33	32.43**	22.50**	41.06**	36.45**	81.59**	51.11**	23.65**	18.32**

*** and ** significant at 0.05 and 0.01 levels of probability, respectively.**

Table (18): Heterosis values relative to mid parent and better parent for yield and its components in rice.

Genotypes	No. of panicles/ plant		Panicle length (cm)		Panicle weight (g)		Spiklete fertility		1000 grain weight (g)		Grain yield/ plant (g)		Harvest index %	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
Sakha104x IHL17	10.00**	6.94**	2.39**	1.63**	10.16**	4.02**	4.64**	1.65**	8.97**	5.44**	4.68**	3.93**	2.55**	1.15
Sakha104x IHL65	16.03**	5.56**	9.41**	3.53**	11.30**	1.35**	2.95**	0.26	4.26**	-4.27**	8.02**	4.77**	8.62**	5.56**
Sakha104x IHL175	18.40**	2.78**	3.50**	0.50*	20.41**	5.06**	11.60**	9.78**	6.37**	1.37*	6.84**	0.82	7.41**	2.45**
Sakha104xSuper303	5.56**	5.56**	7.70**	1.70**	15.38**	10.10**	5.15**	1.27*	4.59**	-2.95**	3.73**	-1.46	11.43**	6.04**
Sakha106x IHL17	10.61**	7.35**	0.87**	-0.75**	9.77**	8.75**	2.12**	1.68**	11.28**	9.87**	1.25	0.86	10.89**	3.11**
Sakha106x HL65	21.95**	17.19**	-2.29**	-5.42**	18.58**	13.08**	3.19**	3.00**	8.63**	1.65*	6.84**	4.75**	6.05**	2.70**
Sakha106x IHL175	36.75**	25.00**	6.04**	5.40**	27.94**	16.61**	8.92**	4.57**	17.45**	14.17**	18.95**	11.09**	9.10**	7.67**
Sakha106xSuper303	7.35**	1.39*	-1.34**	-4.70**	20.54**	9.83**	0.65	-0.67	7.12**	1.33*	10.91**	4.27**	11.49**	0.24
GZ11332x IHL17	11.29**	1.47**	6.93**	2.02**	-6.74**	-7.26**	3.03**	2.83**	6.31**	1.17	20.27**	18.89**	16.35**	12.97**
GZ11332x IHL65	18.26**	15.25**	8.78**	8.64**	18.83**	14.97**	2.26**	1.81**	4.92**	4.40**	21.49**	17.33**	7.19**	5.82**
GZ11332x IHL175	26.61**	23.21**	1.29**	-1.25**	4.28**	-3.64**	8.16**	3.23**	6.12**	2.53**	13.95**	7.98**	3.74**	0.49
GZ11332xSuper303	10.94**	-1.39*	10.15**	9.77**	8.52**	-2.44**	2.29**	1.57**	5.58**	4.90**	16.32**	10.97**	8.07**	1.29
Sakha101x IHL17	9.49**	8.70**	3.80**	2.87**	8.37**	0.25*	1.44**	0.35	5.63**	4.84**	-8.37**	-12.58**	5.60**	3.17**
Sakha101x IHL65	12.50**	4.35**	-2.70**	-6.48**	-7.74**	-17.62**	2.61**	1.25*	3.80**	-0.99	8.61**	1.32	1.60*	-0.32
Sakha101x IHL175	16.39**	2.90**	1.80**	0.46*	16.89**	0.11	4.94**	-0.69	4.44**	3.57**	0.07	-1.77*	-8.31**	-11.71**
Sakha101xSuper303	-3.55**	-5.56**	8.24**	3.82**	11.40**	8.58**	1.49**	1.30*	5.64**	1.89**	8.64**	7.38**	7.22**	1.09
Sakha108x IHL17	4.29**	1.39*	3.36**	2.12**	19.47**	19.23**	1.16*	0.56	6.03**	3.76**	28.62**	24.44**	25.00**	14.01**
Sakha108x IHL65	12.98**	2.78**	6.72**	2.89**	21.36**	17.00**	2.31**	1.46**	4.09**	0.66	30.48**	29.22**	14.70**	0.73
Sakha108x IHL175	10.40**	-4.17**	4.99**	3.93**	40.95**	29.80**	6.51**	1.27*	4.02**	3.41**	17.98**	7.23**	12.43**	-2.87**
Sakha108xSuper303	13.89**	13.89**	13.74**	9.43**	20.75**	8.91**	2.56**	2.24**	12.47**	9.99**	30.63**	19.49**	51.42**	42.91**
Sakha109x IHL17	32.28**	23.53**	13.00**	7.19**	33.34**	28.11**	3.80**	3.07**	15.30**	11.65**	37.13**	35.57**	48.31**	33.99**
Sakha109x IHL65	22.03**	22.03**	4.47**	3.97**	9.14**	1.06**	0.96*	0.01	2.88**	0.55	9.63**	8.29**	17.26**	2.04*
Sakha109x IHL175	42.86**	35.59**	13.08**	9.59**	33.91**	18.69**	7.90**	2.48**	12.36**	10.50**	26.55**	17.37**	36.85**	17.17**
Sakha109xSuper303	41.98**	29.17**	23.39**	23.06**	21.75**	14.19**	3.04**	2.85**	11.04**	9.76**	37.93**	28.76**	64.84**	54.03**

*** and ** significant at 0.05 and 0.01 levels of probability, respectively.**

Table (19): Heterosis values relative to mid parent and better parent for quality traits in rice.

Genotypes	Hulling %		Milling %		Head rice recovery		Grain shape	
	MP	BP	MP	BP	MP	BP	MP	BP
Sakha104x IHL17	0.81	0.41	2.79**	1.82**	10.41**	0.13	26.21**	21.62**
Sakha104x IHL65	2.78**	1.86**	1.80**	1.17**	11.60**	-0.83**	29.51**	19.45**
Sakha104x IHL175	1.17*	1.13*	0.14	-1.07**	11.37**	7.70**	41.41**	27.99**
Sakha104xSuper303	1.95**	1.32*	1.79**	0.65	3.49**	-0.33	19.30**	9.86**
Sakha106x IHL17	2.32**	0.69	1.97**	1.65**	11.68**	2.08**	20.93**	5.89**
Sakha106x HL65	2.08**	-0.04	-1.27**	-3.10**	12.77**	0.97**	-17.63**	-19.31**
Sakha106x IHL175	1.90**	0.71	2.35**	2.30**	7.73**	5.04**	2.13**	2.13**
Sakha106xSuper303	5.11**	4.48**	-0.09	-0.23	4.34**	1.32**	1.58**	-0.33**
GZ11332x IHL17	-3.79**	-3.81**	1.58**	1.42**	16.56**	8.50**	3.24**	-6.07**
GZ11332x IHL65	1.34**	0.80	1.83**	0.41	15.96**	5.69**	7.16**	4.78**
GZ11332x IHL175	1.29**	0.88	-0.02	-0.44	5.81**	5.22**	6.92**	2.45**
GZ11332xSuper303	1.22*	0.22	1.86**	1.53**	4.41**	3.38**	49.13**	45.58**
Sakha101x IHL17	0.36	-0.35	0.98**	0.94**	8.84**	-0.18	31.44**	16.25**
Sakha101x IHL65	1.28**	0.06	1.55**	-0.07	11.25**	-0.06	-5.33**	-6.20**
Sakha101x IHL175	0.82	0.53	1.21**	0.98**	2.08**	-0.09	7.12**	5.89**
Sakha101xSuper303	-0.83	-1.12*	3.79**	3.66**	-5.63**	-8.02**	40.59**	39.53**
Sakha108x IHL17	1.19*	0.98	3.82**	2.21**	9.27**	6.50**	32.97**	15.15**
Sakha108x IHL65	0.10	-0.62	2.73**	-0.42	22.12**	16.42**	5.03**	1.59**
Sakha108x IHL175	-0.18	-0.40	2.42**	1.10**	2.12**	-2.07**	-0.81**	-2.07**
Sakha108xSuper303	1.20*	0.40	4.39**	2.94**	-0.64**	-4.33**	7.49**	4.15**
Sakha109x IHL17	1.00*	0.23	3.01**	2.74**	25.83**	21.57**	24.51**	9.41**
Sakha109x IHL65	1.40**	0.12	0.33	-1.49**	29.71**	28.18**	24.83**	22.77**
Sakha109x IHL175	1.08*	0.74	1.81**	1.81**	17.54**	6.52**	5.67**	5.24**
Sakha109xSuper303	4.21**	3.95**	4.25**	4.15**	15.03**	4.64**	34.00**	32.01**

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

4.4. Correlation coefficient between grain yield and related components as well as some morphophysiological and quality traits.

Correlation coefficient recorded between grain yield and days to 50% heading(days), chlorophyll content, harvest index, number of panicle per plant, 1000 grain weight, hulling, milling, head rice recoveary, grain shape are shown in Table 20.

Results indicated that there were highly significant and positive correlation values between grain yield/ plant and each of chlorophyll content, harvest index, number of panicle per plant, 1000 grain weight, and grain shape.

Also, negative and significant correlation values were detected between days to 50% flowering and each of chlorophyll content, harvest index, number of panicle /per plant, and head rice recoveary.

Significantly positive correlation values were observed between chlorophyll content and each of harvest index, number of panicle/ per plant, milling, and head rice recoveary.

Meantime, significant and positive correlation values were detected between harvest index and each number of panicle/ plant, 1000 grain weight, milling, and head rice recoveary.

Number of panicle per plant had significant and positive correlation values with head rice recoveary.

Also, significant and positive correlation values were obtained between hulling and milling**. Kumar et al., (2022) and Kumar et al., (2024**) who found that Significant negative correlations were observed with days to 50% flowering and 1000-grain weight. Number of fertile grains panicle-1 was positively and significantly associated with grain yield plot.

Table 20: Correlation coefficient between grain yield and some related components trait, morphophysiological and quality traits.

	X1	X2	X3	X4	X5	X6	X7	X8	X9
X1	1.000								
X2	-0.569**	1.000							
X3	-0.349*	0.651**	1.000						
X4	-0.387*	0.516**	0.578**	1.000					
X5	-0.131	0.322	0.442*	0.264	1.000				
X6	-0.065	0.195	0.318	0.314	0.292	1.000			
X7	-0.066	0.479**	0.402*	0.285	0.297	0.373*	1.000		
X8	-0.488**	0.497**	0.536**	0.453**	0.126	0.149	0.209	1.000	
X9	-0.220	0.264	0.242	0.264	0.230	0.185	0.331	0.171	1.000
Y	-0.338	0.655**	0.705**	0.571**	0.497**	0.154	0.325	0.327	0.444*

*** and ** significant at 0.05, and 0.01 levels of probability, respectively.**

X1 = Days to 50% heading(days)‹X2= chlorophyll content‹ X3= Harvest index, X4= Number of panicle per plant‹X5 =1000 grain weight‹X6= hulling, X7= milling‹X8= head rice recoveary‹X9= Grain shape‹y= yield

SUMMARY AND CONCLUSION

5-SUMMARY AND CONCLUSION

This work was undertaken at the Farm of Rice Research and Training Center. (RRTC), Sakha, Kafr El-Sheikh, Egypt, to investigate the gene action of some morphophysiological, yield and its attributing traits as well as quality traits during 2023 and 2024 seasons. The plant materials of this work included six parental varieties, i.e., Sakha104, Sakha106, GZ11332, Sakha108, Sakha109, Sakha101 and 4 testers Viz., IHL17, IHL65, IHL175, Super303 of rice.

In 2023 season, the ten parent 's grains were sown. After thirty days old seedlings of each parent were individually transplanted in the permanent field in 10 rows. Each row was 5 meters long and 20×20cm apart between plants and rows. The row contained 25 hills. During this season after heading, the six lines were crossed with the four testers to produce 24 F1 crosses using bulk emasculation conducted using the hot water method (42-44 °C for 10 min) .

In summer season 2024, the parental lines and their F1 crosses were sown. Thirty days after sowing, the seedlings of 34 genotypes of rice (10 parents and 24 F1crosses) were transplanted and set in a randomized complete block design (RCBD) with three replications.

Data were recorded on six morphophysiological traits (days to 50% heading, plant height, No. of tillers plant-1, flag leaf area, flag leaf angle, and chlorophyll content), seven yield traits (No. of panicle plant-1, panicle length, panicle weight, spikelet fertility, 1000 grain weight, grain yield plant-1, and harvest index) , and four quality traits (hulling%, milling%, head rice recovery, and grain shape). Combining ability was estimated according to **Kempthorne (1954).** The results obtained could be summarized as follows:

A. Analysis of variance and mean performance

A.1. Morphophysiological traits

The mean squares of genotypes and their partitions were significant for the six morphophysiological traits. For days to 50% heading, the parent Sakha106 exhibited the lowest mean value, while the cross Sakha108xIHL65 expressed the most desirable effects. For plant height, the cross Sakha101xSuper303 was the best among all crosses since it had the lowest significant mean value for this trait. For number of tillers plant-1, the most desirable mean value was detected for the cross Sakha 109xSR303. Regarding flag leaf area, flag leaf angle and chlorophyll content, the cross Sakha109xSuper303 exhibited the most desirable mean value.

A.2. Yield and its attributed traits

Mean squares of seven yield traits viz, No. of panicle plant-1, panicle length, panicle weight, spikelet fertility, 1000 grain weight, grain yield plant-1, and harvest index were significant for all genotypes studied. The cross Sakha109xSuper303 was the best one among all studied genotypes since it expressed the best mean values for No. of panicles plant, panicle length, panicle weight, spikelet fertility, grain yield plant and harvest index. The cross Sakha108xSuper303 was the best one for 1000 grain weight.

A.3. Grain quality traits

Mean squares of genotypes and their partitions were significant for all quality traits studied. The cross Sakha104xIHL65 was the best among all genotypes because it exhibited the best mean values for hulling% and milling%. Moreover, the most desirable mean values for head rice recovery and grain shape were recorded by the cross Sakha104xIHL175 and GZ11332xSuper303, respectively.

B. Combining ability analysis

B.1 Morphophysiological traits

For each morphophysiological trait, the mean squares resulting from specific combining ability (SCA) were significant and greater than those resulting from general combining ability GCA, demonstrating the significance of non-additive gen action in controlling these traits. The best general combiners were detected for the parents Sakha104 for days to 50% heading, GZ11332 for chlorophyll content, the parent Sakha 101 for plant height and the parent Sakha109 for No. of tillers plant, flag leaf area, and flag leaf angle. The tester IHL17 was the best combiner for days to 50% heading, while the tester super 303 was the best combiner for plant height, flag leaf area, flag leaf angle and chlorophyll content. The cross Sakha109xSuper303 expressed the best SCA effects for days to 50^ heading, No. of tillers plant-1 and chlorophyll content. The crosses Sakha101x super 303, Sakha108xIHL65, and Sakha101xIHL65 gave the best SCA effects for plant height, flag leaf area, and flag leaf angle, respectively.

B.2 Yield and its attributing traits

Yield and its associated qualities were inherited due to non-additive gene activity. Given that it exhibited the greatest and positive GCA for every characteristic examined, the parent variety Sakha109 appeared to be the best general combiner and the tester super303 was the best among all studied testers because it expressed the highest GCA effects for all traits except panicle length. The tester IHL17 was the best for panicle length. The most desirable SCA effects were detected in the crosses Sakha109xSuper303 for No. of panicle plant-1, the cross Sakha106xIHL175for panicle length and grain yield plant-1, the cross GZ11332xIHL65 for panicle weight, the cross Sakha101xIHL65 for spikelet fertility, the cross Sakha108xSuper 303 for 1000 grain weight and harvest index.

B.3 Grain Quality traits

The significance of dominance and epistasis gene action in regulating quality attributes was demonstrated by the significantly greater mean squares resulting from specific combining ability (SCA) compared to general combining ability (GCA). The parent variety Sakha104 was the best combiner for hulling%, milling% and head rice recovery, while the parent Sakha 109 was the highest combiner for grain shape. The tester IHL65 was the best for hulling% and milling%, whereas the best testers for head rice recovery and grain shape were IHL175 and Super303, respectively. The most desirable SCA effects were obtained by crosses Sakha108xIHL17 for hulling% and head rice recovery. The highest SCA effects for milling% and grain shape were detected by the crosses Sakha106xIHL175 and GZ11332xSuper303, respectively.

C- Heterosis for mid parent (MP) and better parents (BP)

C.1 Morphophysiological traits

The most desirable heterosis for earliness was detected for the crosses Sakha104xIHL17 relative to Mid-Parent and the cross Sakha108xIHL relative to better-P. For plant height, the best heterosis relative to Better-Parent was obtained by the cross Sakha101xSR303. The best heterosis relative to both types was detected by the crosses GZ11332xIHL175 for No. of tiller plant-1, Sakha108xIHL65 for chlorophyll content, Sakha109xIHL17 for flag leaf angle, and Sakha109xSR303 for flag leaf area.

C.2 Yield and its attributing traits

The most desirable heterotic effects relative to mid-parent and better parent were detected by the crosses Sakha109xIHL175 for No. of panicles plant-1, Sakha109xSR303, for panicle length, and harvest index, Sakha108xIHL175 for panicle weight, Sakha104xIHL175 for spikelet fertility, Sakha106xIHL65 for 1000 grain weight. For grain yield plant-1, the best heterotic effects were obtained by cross Sakha109xSuper303 relative to mid parent and the cross Sakha109xIHL17 relative to better parent.

C.3 Grain quality traits

The highest heterosis relative to Mid-Parent and better -Parent were detected by crosses Sk106xSR303 for hulling%, the cross Sakha109xIHL65 for head rice recovery, and the cross GZ11332xSuper303 for grain shape. With regard to milling%, the best heterotic effect was detected by the cross Sakha109xSR303 relative to mid parent and the cross Sakha109xIHL65 relative to better parent.

Conclusion:

From the previous results, the line Saka 109 and tester Super 303 were the best parent. The cross Sakha 109 × Super 303 was the most desirable value for grain yield plant and most of its attribute traits. As a result, this cross is promising and may be applied in upcoming rice breeding initiatives to improve yield potentiality and quality.

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ARABIC SUMMARY

الملخص العربي

أجريت هذه الدراسة لتحديد الفعل الجيني وقوة الهجين لمجموعة من الصفات المورفوفسيولوجية والمحصولية وكذلك صفات الجودة في مجموعة من هجن الأرز ناتجة من التهجين بين ستة أباء وأربعة كشافات بنظام السلالة × الكشاف. واشتملت التراكيب الوراثية المستخدمة على ستة أباء من الأرز على درجة عالية من التباين الوراثي وهي سخا 101، سخا 104، جي زد 11332، سخا 106، سخا 108، سخا 109، واشتملت الدراسة على أربع كشافات هي: IHL17، IHL65، IHL175، Super303. واجريت الدراسة بالمزرعة البحثية التابعة لمركز البحوث والتدريب في الأرز (RRTC)، بمحطة البحوث الزراعية بسخا خلال موسمي 2023، 2024. ففي موسم 2023 تم التهجين بين السلالات الأبوية والكشافات وتم الحصول على 24 هجين. وفى موسم 2024 تم تقييم الهجن الناتجة مع الأباء العشرة في تصميم قطاعات كاملة العشوائية باستخدام ثلاث مكررات. وتم تسجيل الصفات التالية:

أ- صفات مورفوفسيولوجية:

1. ميعاد خروج 50% من السنابل
2. ارتفاع النبات
3. عدد الفروع للنبات
4. مساحة ورقة العلم
5. وزاوية ورقة العلم
6. محتوى الأوراق من الكلوروفيل

ب- صفات محصولية:

1. عدد الداليات لكل نبات
2. طول الدالية
3. وزن الدالية
4. نسبة الخصوبة
5. وزن 1000 حبة

6. محصول الحبوب للنبات
7. دليل الحصاد

ج- صفات الجودة

1. نسبة التقشير
2. نسبة التبييض
3. نسبة الحبوب السليمة في الأرز
4. شكل الحبوب

وتم تقدير القدرة العامة والخاصة على التآلف طبقا لطريقة Kempthorne (1954)، وكذلك تم تقدير قوة الهجين منسوبة الى متوسط الأبوين وأفضل الأبوين لكل الصفات تحت الدراسة.

ويمكن تلخيص أهم النتائج المتحصل عليها فيما يلي:

أ- تحليل التباين ومتوسط سلوك الصفات

أ.1 الصفات المورفوفسيولوجية

كان التباين الراجع الى التراكيب الوراثية وكذلك السلالات الأبوية والكشافات والتفاعل بينهم معنويا لجميع الصفات تحت الدراسة والتي اشتملت على ميعاد خروج 50% من طرد السنابل، ارتفاع النبات، عدد الفروع للنبات، مساحة ورقة العلم، وزاوية ورقة العلم، محتوى الأوراق من الكلوروفيل. وأمكن الحصول على أفضل القيم لصفة ميعاد طرد السنابل من الصنف سخا 106وكذلك الهجين Sakha108xIHL65. وأعطى الهجين سخا 101× سوبر 303أفضل القيم لصفة ارتفاع النبات والهجين سخا 109× سوبر 303لصفة عدد فروع النبات والهجين سخا109× سوبر 303 لصفات مساحة ورقة العلم وزاوية ورقة العلم ومحتوى الأوراق من الكلوروفيل.

أ.2 المحصول ومكوناته

كان التباين الراجع الى التراكيب الوراثية ومكوناتها المختلفة معنويا لجميع الصفات تحت الدراسة والتي اشتملت على عدد الداليات لكل نبات، طول الدالية، وزن الدالية، نسبة

الخصوبة وزن 1000 حبة، محصول الحبوب للنبات، دليل الحصاد مما يدل على وجود اختلافات وراثية كثيرة بين الأباء المستخدمة في هذه الدراسة. وأعطى الهجين سخا109× سوبر 303أفضل المتوسطات لصفات عدد داليات للنبات، طول الدالية، وزن الدالية، نسبة الخصوبة، محصول الحبوب للنبات ودليل الحصاد، بينما أعطى الهجين سخا108× سوبر 303أفضل القيم لوزن 1000 حبة.

أ.3 صفات الجودة

كان التباين الراجع الى التراكيب الوراثية ومكوناتها معنويا لجميع صفات الجودة تحت الدراسة (نسبة التقشير، نسبة التبييض، نسبة الحبوب السليمة في الأرز، شكل الحبوب). وأظهرت النتائج أن الهجين Sakha104xIHL65 كان الأفضل بالنسبة لصفتي التقشير والتبييض، بينما أعطى الهجين Sakha104xIHL175 أعلي القيم لصفة نسبة الحبوب السليمة في الأرز والهجين جي زد 11332× سوبر 303لصفة شكل الحبوب.

ب- تحليل القدرة العامة والخاصة على التآلف

ب.1 الصفات المورفوفسيولوجية

كان التباين الراجع الى القدرة الخاصة على التآلف أعلى منه للقدرة العامة على التآلف لصفات ميعاد خروج 50% من طرد السنابل وارتفاع النبات وعدد أفرع النبات ومساحة ورقة العلم وزاوية ورقة العلم ومحتوى الأوراق من الكلوروفيل مما يعنى أهمية الفعل الوراثي غير المضيف في توارث هذه الصفات. وأعطى الصنف سخا 104أفضل تأثيرات للقدرة العامة على التآلف لصفة ميعاد طرد السنابل ومحتوى الأوراق من الكلوروفيل بينما كان الأب سخا 101هو الأفضل لصفة ارتفاع النبات، وأعطى الأب سخا 109أفضل تأثيرات للقدرة العامة على الائتلاف لصفات عدد فروع النبات ومساحة ورقة العلم وزاوية ورقة العلم. واعطى الكشاف IHL17 أفضل تأثيرات للقدرة العامة على التآلف لميعاد خروج 50% من طرد الدليات والكشاف سوبر 303لصفات ارتفاع النبات، مساحة ورقة العلم، وزاوية ورقة العلم ومحتوى الأوراق من الكلوروفيل. وأعطى الهجين سخا109× سوبر 303أفضل تأثيرات للقدرة الخاصة على التآلف لميعاد خروج 50% من طرد السنابل وعدد أفرع النبات ومحتوى الأوراق من الكلوروفيل.

وكان Sakha101xSuper303, Sakha108xIHL65, and Sakha101xIHL65 أفضل تأثيرات للقدرة الخاصة على التألف لصفات ارتفاع النبات ومساحة ورقة العلم وزاوية ورقة العلم، على الترتيب.

ب.2 المحصول ومكوناته

أظهرت النتائج أهمية الفعل الوراثي غير المضيف في توارث صفات المحصول ومكوناته وهي عدد الداليات للنبات، طول الدالية، وزن الدالية، نسبة الخصوبة، وزن 1000 حبة ومحصول الحبوب للنبات ودليل الحصاد. وأعطى الأب سخا 109أفضل تأثيرات للقدرة العامة على التآلف لجميع الصفات تحت الدراسة الخاصة بالمحصول ومكوناته. وأعطى الكشاف سوبر 303أفضل تأثيرات للقدرة العامة على التألف لجميع الصفات ماعدا طول الدالية. وأعطى الكشاف IHL17 أفضل التأثيرات لصفة طول الدالية. وأعطى الهجين سخا109× سوبر 303 أفضل تأثيرات للقدرة الخاصة على التآلف لصفة عدد أفرع النبات وأعطى الهجين SK106xIHL175 أفضل التأثيرات لصفتي طول الدالية ومحصول الحبوب للنبات، واعطى الهجين GZ11332xIHL65 أفضل تأثيرات للقدرة الخاصة على التآلف لوزن الدالية واعطى الهجين SK101xIHL65 أفضل القيم لنسبة الخصوبة والهجين سخا 108× سوبر 303لصفتي وزن 1000 حبة ودليل الحصاد بينما كان الهجين سخا109×سوبر303هو الأفضل بالنسبة للقدرة على التآلف لصفة عدد داليات النبات.

ب.3 صفات الجودة

كان التباين الراجع للقدرة الخاصة على التآلف هو الأكثر اهمية من التباين الراجع للقدرة العامة على التآلف لصفات التقشير والتبييض ونسبة الحبوب السليمة وشكل الحبوب، مما يعنى أهمية الفعل الوراثي غير المضيف في توارث صفات الجودة تحت الدراسة. وأوضحت الدراسة أن الصنف الأبوي سخا 104هو الأفضل من جهة تأثيرات القدرة العامة على التألف لصفات نسبة التقشير ونسبة التبييض والحبوب السليمة، بينما كان الآب سخا109 هو الافضل لصفة شكل الحبوب. وأعطى الكشاف IHL65 أفضل تأثيرات للقدرة العامة على التألف لصفتي نسبة التقشير ونسبة التبييض، بينما كان الكشافات IHL175K, SR303 هما الأفضل لصفتي الحبوب السليمة وشكل الحبوب، على الترتيب. وأعطى الهجين SK108xIHL17 أفضل تأثيرات للقدرة الخاصة على التألف لصفتي نسبة التقشير والحبوب

السليمة. وأعطى الهجين SK106xIHL175 أعلي تأثيرات لصفة نسبة التبييض والهجين جي زد 11332× سوبر 303 أفضل التأثيرات لصفة شكل الحبوب.

جـ قوة الهجين

جـ.1 الصفات المورفوفسيولوجية

أمكن الحصول على أفضل قوة هجين لصفة ميعاد خروج 50% من طرد السنابل في الهجين SK104xIHL17 نسبة الى متوسط الابوين والهجين SK108xIHL65 نسبة الى أفضل الأبوين. وبالنسبة لارتفاع النبات، فإن الهجين سخا101× سوبر303قد أعطى أفضل قوة هجين نسبة الى أفضل الابوين. أما أفضل قوة هجين نسبة الى متوسط الأبوين وأفضل الأبوين معا فقد تم الوصول اليها مع الهجين GZ11332xIHL175 لصفة عدد أفرع النبات والهجين SK108xIHL65 لمحتوى الأوراق من الكلوروفيل والهجين SK109xIHL17 لصفة زاوية ورقة العلم، والهجين سخا109×سوبر303 لصفة مساحة ورقة العلم.

جـ.2 المحصول ومكوناته

أعطى الهجين SK109xIHL175 أفضل قيم لقوة الهجين نسبة الى متوسط الأبوين وأفضل الأبوين لصفة عدد داليات النبات، وأعطى الهجين سخا109× سوبر303 أفضل القيم لقوة الهجين لصفتي طول الدالية ودليل الحصاد. واعطى الهجين SK108xIHL175 أفضل التأثيرات لوزن الدالية، والهجين SK104xIHL175 لصفة نسبة الخصوبة، والهجين SK106xIHL65 لوزن 1000 حبة. وبالنسبة لمحصول الحبوب للنبات فقد أمكن الحصول على تأثيرات مرغوبة لقوة الهجين مع الهجين سخا109× سوبر303 نسبة الى متوسط الأبوين ومع الهجين SK109xIHL17 نسبة الى أفضل الأبوين.

جـ.3 صفات الجودة

أمكن الحصول على أفضل قيم لقوة الهجين نسبة الى متوسط الأبوين وأفضل الأبوين مع الهجين سخا106×سوبر303لصفة نسبة التقشير، والهجين SK109xIHL65 لصفة نسبة الحبوب السليمة للأرز، والهجين جي زد 11332× سوبر303 لصفة شكل الحبوب. وبالنسبة لصفة التبييض فأمكن الحصول على أفضل تأثيرات لقوة الهجين نسبة الى متوسط الابوين مع الهجين سخا109×سوبر303 وبالنسبة الى أفضل الأبوين مع الهجين SK109xIHL65

الملخص العربى

كليـــة الزراعـــة
FACULTY OF AGRICULTURE

التحسين الوراثي للمحصول وصفات الجودة في بعض الهجن القمية في الأرز

رسالة مقدمة من

ناديه عاطف إبراهيم عبد الله تعلب

بكالوريوس العلوم الزراعية (محاصيل) كلية الزراعة - جامعة بنها (٢٠٢٢م)

كجزء من متطلبات الحصول على درجة

الماجستير في العلوم الزراعية

تخصص (تربية محاصيل)

من قسم المحاصيل

لجنــة الفحص والمناقشة

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أستاذ تربية المحاصيل المتفرغ- كلية الزراعة – جامعة بنها

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تاريخ المناقشة: ٢٥/ ١٠ / ٢٠٢٥

وكيل الكلية للدراسات العليا والبحوث — **عميد الكلية**

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٢٠٢٥

كليـــــة الزراعـــــة
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الكلية معتمده بالقرار (154) بتاريخ 2016/5/23

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رسالة مقدمة من

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كجزء من متطلبات الحصول على درجة الماجستير في العلوم الزراعية

تخصص (تربية محاصيل)

من قسم المحاصيل

كلية الزراعة بمشتهر
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